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[illegible]

R35464 = Nucleic acid sequence of EST R35464 (SEQ ID NO: 12)
ORF = EST R35464 Open Reading Frame Translation (SEQ ID NO: 13)

R35464 = Nucleic acid sequence of EST R35464 (SEQ ID NO: 12)
ORF = EST R35464 Open Reading Frame Translation (SEQ ID NO: 13)

FIGURE 2

R74593	GCAATAATTA CCTGACCAAG GAGGAGTGCC TCAAGAAATG TGCCACTGTC	50
ORF	Q * L P D Q G G V P Q E M C H C H	17
R74593	ACAGAGAATG CCACGGGTGA CCTGGCCACC AGCAGGAATG CAGCGGATTC	100
ORF	R E C H G * P G H Q Q E C S G F	33
R74593	CTCTGTCCCA AGTCTCCCAG AAGGCAGGAT TCTGAAGACC ACTCCAGCGA	150
C F	L C P K S P R R Q D S E D H S S D	50
R74593	TATGTTCAAC TATGAAGAAT ACTGCACCGC CAACGCAGTC ACTGGGCCTT	200
ORF	M F N Y E E Y C T A N A V T G P C	67
R74593	GCCGTGCATC CTTCCACGCG TGGTACTTTG ACGTGGAGAG GAACTCCTGC	250
ORF	R A S F P R W Y F D V E R N S C	83
R74593	AATAACTTCA TCTATGGAGG CTGCCGGGGC AATAAGAACA GCTACCGCTC	300
ORF	N N F I Y G G C R G N K N S Y R S	100
R74593	TGAGGAGGCC TGCATGCTCC GCTGCTTCCG CCAGCAGGAG AATCCTCCCC	350
ORF	E E A C M L R C F R Q Q E N P P L	117
R74593	TGCCCCCTTG CTCAAAGGTG GTGGTTCTGG CCGGGGCTGT TTCGTGATGG	400
ORF	P L G S K V V V L A G A V S * W	133
R74593	TGTTGATCCT TTTCTGGGG AGCNTCCATG GTCTTACTGA TTCCGGGTGG	450
ORF	C * S F S W G A S M V L L I P G G	150
R74593	CAAGGAGGAA CCAGGAGCGT GCCCTGCGGA NCGTCTGGAG CTTCGGAGAT	500
ORF	K E E P G A C P A X R L E L R R *	167
R74593	GACAAGGGNT	510
ORF	Q G	169

KEY

R74593 = Nucleic acid sequence of EST R74593 (SEQ ID NO: 14)

ORF = EST R74593 Open Reading Frame Translation (SEQ ID NO: 15)

FIGURE 3

3

R35464	GGCCGGGTCGT	TTCTCGCCTG	GCTGGGA-TC	GCTGCTCCTC	TCTGGGGTCC	50												
N39798			TGGGANTC	GCTGCTCCTC	TCTGGGGTCC	28												
H94519	GCNGCG-CGT	TNNTCGCNT-	GCTGGGA-TC	GCTGCACCTC	TCTGGGGTCC	47												
R74593 corr.	-----	-----	-----	-----	-----													
Consensus	GGCCGGGTCGT	TTCTCGCCTG	GCTGGGA-TC	GCTGCTCCTC	TCTGGGGTCC	50												
Translation	A	G	S	F	L	A	W	L	G	S	L	L	L	S	G	V	-3	
R35464	TGGCCGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGAA	100												
N39798	TGG-CGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGAA	77												
H94519	NGG-CGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGAA	96												
R74593 corr.	-----	-----	-----	-----	-----													
Consensus	TGG-CGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGAA	99												
Translation	L	A	A	D	B	E	B	S	I	H	D	E	C	L	V	S	K	15
R35464	GGTGGTGGGC	AGATTCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	150												
N39798	GGTGGTGGGC	AGATGCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	127												
H94519	GGTGGTGGGC	AGATGCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	146												
R74593 corr.	-----	-----	-----	-----	-----													
Consensus	GGTGGTGGGC	AGATGCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	149												
Translation	V	V	G	B	C	B	A	S	M	E	B	H	H	X	N	V	T	32
R35464	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	200												
N39798	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	177												
H94519	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	196												
R74593 corr.	-----	-----	-----	-----	-----GC	2												
Consensus	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	199												
Translation	D	G	S	C	D	L	E	V	X	G	G	C	D	G	N	S	48	
R35464	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	250												
N39798	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	227												
H94519	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	246												
R74593 corr.	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	52												
Consensus	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	249												
Translation	N	N	Y	L	T	K	E	E	C	L	K	K	C	A	T	V	T	65
R35464	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	300												
N39798	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	277												
H94519	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	296												
R74593 corr.	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	102												
Consensus	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	299												
Translation	E	N	A	T	G	D	L	A	T	S	R	N	A	A	D	S	S	32
R35464	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CTGAAGACC	ACTCCAGCGA	350												
N39798	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTCCAGCGA	326												
H94519	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTCCAGCGA	345												
R74593 corr.	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTCCAGCGA	131												
Consensus	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTCCAGCGA	348												
Translation	V	P	S	A	P	R	R	Q	D	S	E	D	H	S	S	D	99	
R35464	TATGTTTCAA	NTATTGNAAG	AATAATTGCA	CCGNCAACGN	ATT-----	393												
N39798	TATGTT-CAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	392												
H94519	TATGTT-CAA	CTA-TG-AAG	AATACTGGCA	CCGCCAACGC	ATTCACTGGG	392												
R74593 corr.	TATGTT-CAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	197												
Consensus	TATGTT-CAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	394												
Translation	M	F	N	Y	E	E	Y	C	T	A	N	A	V	T	G	100		

FIGURE 3 (CONT)

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R35464	-----	-----	-----	-----	-----	
N39798	CCTTGC-GTG	GAATCCTTTC	CCACGCTGGN	AATTNGACG	TTGAGAAGGA	421
H94519	CCT-GC-GTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GNCG	-----	427
R74593 corr.	CCTTGCCGTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GACG	TGGAGA-GGA	243
Consensus	CCTTGCCGTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GACG	TGGAGA-GGA	440
Translation	P C R A	S F	P R W Y	F D V	E R N	129
R35464	-----	-----	-----	-----	-----	
N39798	AC-----	-----	-----	-----	-----	423
H94519	-----	-----	-----	-----	-----	
R74593 corr.	ACTCCTGCAA	TAACTTCATC	TATGGAGGCT	GCCGGGGCAA	TAAGAACAGC	293
Consensus	ACTCCTGCAA	TAACTTCATC	TATGGAGGCT	GCCGGGGCAA	TAAGAACAGC	490
Translation	S C N	N F I	Y G G C	R G N	K N S	145
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	TACCGCTCTG	AGGAGGCCTG	CATGCTCCGC	TGCTTCCGCC	AGCAGGAGAA	343
Consensus	TACCGCTCTG	AGGAGGCCTG	CATGCTCCGC	TGCTTCCGCC	AGCAGGAGAA	540
Translation	Y R S E	E A C	M L R	C F R Q	Q E N	162
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	TCCTCCCTG	CCCCTTGGCT	CAAAGGTGGT	GGTTCTGGCC	GGGGCTGTTT	393
Consensus	TCCTCCCTG	CCCCTTGGCT	CAAAGGTGGT	GGTTCTGGCC	GGGGCTGTTT	590
Translation	P P L	P L G S	K V V	V L A	G A V S	179
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	CGTGATGGTG	TTGATCCTTT	TCCTGGGGAG	CNTCCATGGT	CTTACTGATT	443
Consensus	CGTGATGGTG	TTGATCCTTT	TCCTGGGGAG	CNTCCATGGT	CTTACTGATT	640
Translation	* W C	* S F	S W G A	S M V	L L :	195
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	CCGGGTGGCA	AGGAGGAACC	AGGAGCGTGC	CCTGCCGANC	GTCTGGAGCT	493
Consensus	CCGGGTGGCA	AGGAGGAACC	AGGAGCGTGC	CCTGCCGANC	<u>GTCTGGAGCT</u>	690
Translation	P G G K	E E P	G A C	P A * R	L E L	212
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	TCGGAGATGA	CAAGGGNT				511
Consensus	<u>TCGGAGATGA</u>	CAAGGGNT				708
Translation	R R *	Q G				217

KEY

R35464 = Nucleic acid sequence of EST R35464 (SEQ ID NO.: 12)
 N39798 = Nucleic acid sequence of EST N39798 (SEQ ID NO.: 17)
 H94519 = Nucleic acid sequence of EST H94519 (SEQ ID NO.: 16)
 R74593 corr. = Corrected version of (SEQ ID NO.: 14) G at b.p. 114
 Consensus = Nucleic acid sequence for human bikunin (SEQ ID NO.: 9)
 Translation = Amino acid Translation of Consensus (SEQ ID NO.: 10)

Figure 4 A.

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Schematic depicting the overlap of ESTs bearing homology to the cDNA sequence encoding placental bikunin

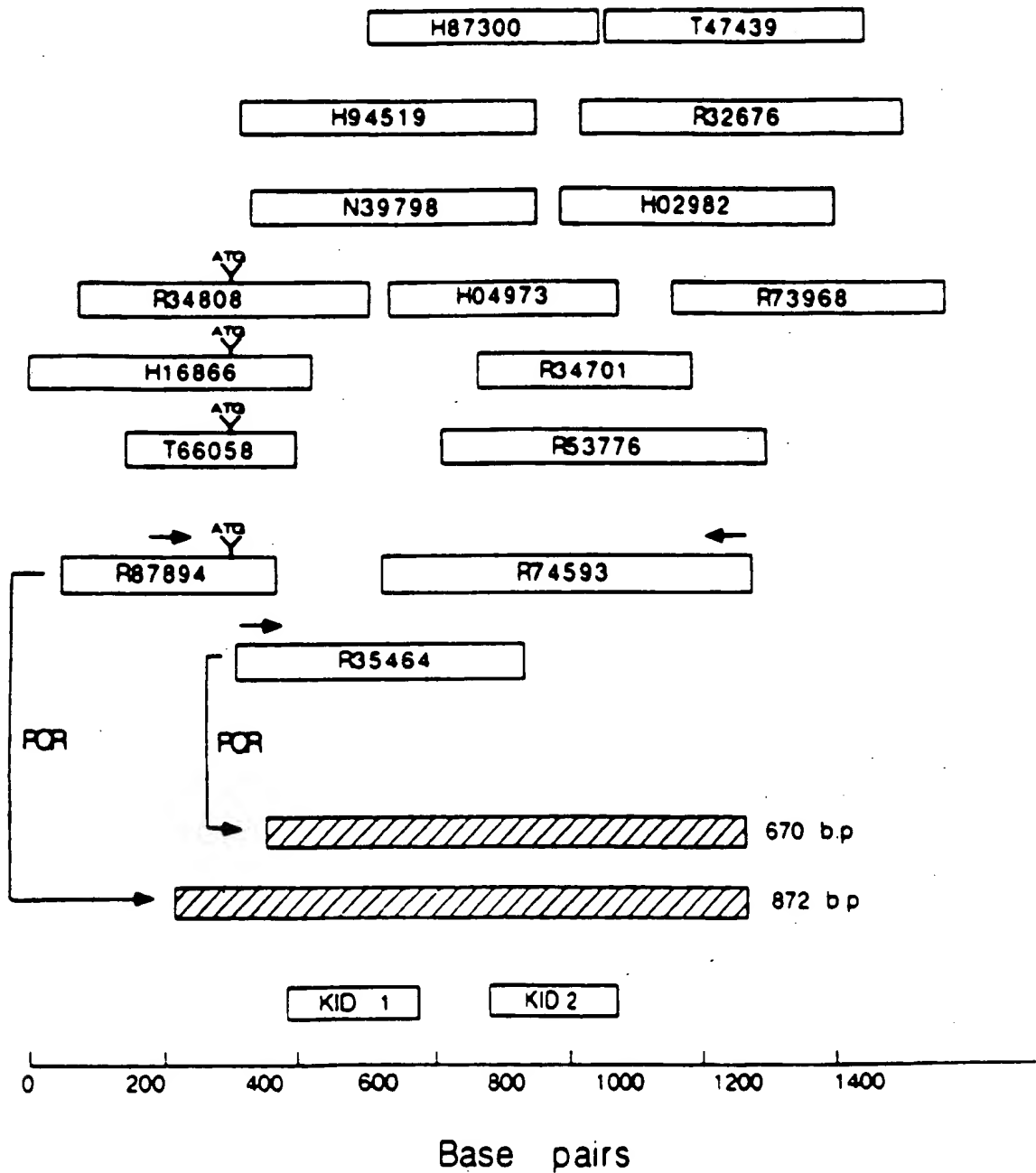
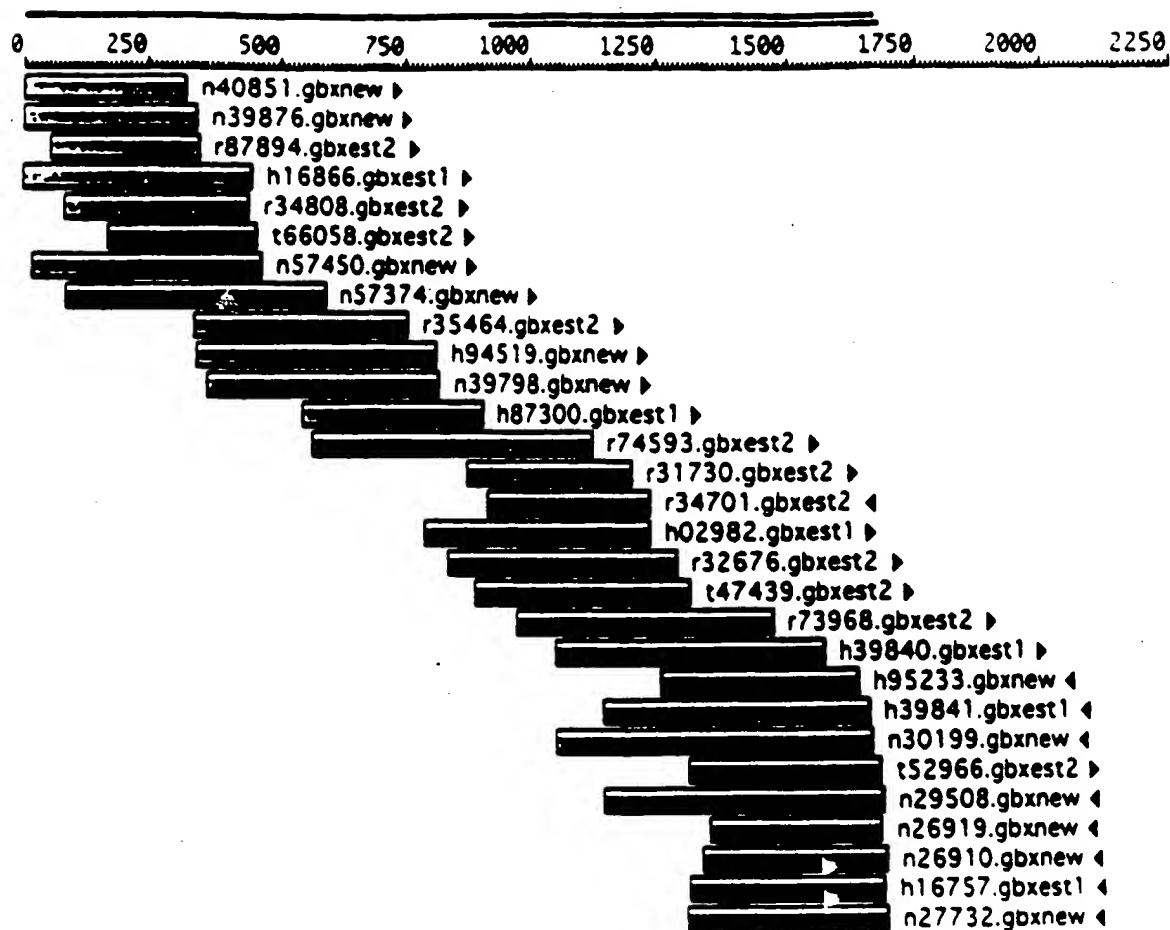


Figure 4B



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Figure 4C

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BikuninGCGA	CCTCCGCGCG	TTGGGAGGTG	TAGCGCGGCT	CTGAACGGCT
N40851GCGA	CCTCCGCGCG	TTGGGAGGTG	TAGCGCGGCT	CTGAACGGCT
N39876GCGA	CCTCCGCGCG	TTGGGAGGTG	TAGCGCGGCT	CTGAACGGCT
R87894
H16866GGCGA	CCTCCGCGCG	TTGGGAGGTG	TAGCGCGGCT	CTGAACGGCT
R34808
T66058
N57450	TAGCGCGGCT	CTGAACGGCT
N57374
R35464
H94519
N39790
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

Figure 4C (Con't)

	5'				3'
Bikunin	GNA	GGGCG	TTGAGTGTCG	CAGGCGGCGA	GGGCGGAGT GAGGAGCAGA
N4085	NGAGNGGCG	TTGAGTGTCG	CAGGCGGCGA	GGGCGGAGT	GAGGAGCAGA
N39876	GCA	GGGCG	TTGAGTGTCG	CAGGCGGCGA	GGGCGGAGT GAGGAGCAGA
R87894	TTGAGTGTCG	NAGGCGGCGA	GGGCGGAGT	GAGGAGCAGA
H16866	..ANGGCG	TTGAGTGTCG	CAGGCGGCGA	GGGCGGAGT	GAGGAGCAGA
R34808G	GAGGAGCAGA
T66058
N57450	GAAGNGGCG	TTGAGTGTCG	CAGGCGGCGA	GGGCGGAGT	GAGGAGCAGA
N57374AGA
R35464
H94519
N39798
H87300
R74593
R31730
R34701
HC2982
R32676
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Figure 4C (C n't)

	101		150
Bikunin	CCCAGGCATC	GGCGCCCGAG	AAGNC.GGGC GTCCCCACAC TGAAGGTCCG
N40851	CCCAGGCATC	GGCGCCCGAG	AAGNC.GGGC GTCCCCACAC TGAAGGTCCG
N39876	CCCAGGCATC	GGCGCCCGAG	AAGNC.GGGC NTCCCCACAC TGAAGGTCCG
R87894	CCCAGGCATC	GGCGCCCGAG	AAGGCCCGGC GTCCCCACAC TGAAGGTCCG
H16866	CCCAGGCATC	GGCGCCCGAG	AAGNC.GGGC GTCCCCACAC TGAAGGTCCG
R34808	CCCAGGCATC	GGCGCCCGAG	AAGNC.GGGC GTCCCCACAC TGAAGGTCCG
T66058
N57450	CCCAGGCATC	GGCGCCCGAG	AAGNC.GGGC GTCCCCACAC TGAAGGTCCG
N57374	CCCAGGCATC	GGCGCCCGAG	AAGNC.GGGC GTCCCCACAC TGAAGGTCCG
R35464
H94519
N39798
H87300
R74593
R31730
R34701
HC2982
R32676
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Figure 4C (Con't)

	151	200
Bikunin	GAAAGGGGAC TTCCGGGGGC TTGGGACCT GGCGGACCCT CCGGGAGCGT	
N40851	GAAAGGGGAC TTCCGGGGGC TTGGGACCT GGCGGACCCT CCGGGAGCGT	
N39876	GAAAGGGGAC TTCCGGGGGC TTGGGACCT GGCGGACCCT CCGGGAGCGT	
R87894	GAAAGGGGAC TTCCGGGGGC TTGGGACCT GGCGGACCCT CCGGGAGCGT	
H16866	GAAAGGGGAC TTCCGGGGGC TTGGGACCT GGCGGACCCT CCGGGAGCGT	
R34808	GAAAGGGGAC TTCCGGGGGC TTGGGACCT GGCGGACCCT CCGGGAGCGT	
T66058 GGACCCT CCGGGAGCGT	
N57450	GAAAGGGGAC TTCCGGGGGC TTGGGACCT GGCGGACCCT CCGGGAGCGT	
N57374	GAAAGGGGAC TTCCGGGGGC TTGGGACCT GGCGGACCCT CCGGGAGCGT	
R35464	
H94519	
N39798	
H87300	
R74593	
R31730	
R34701	
H02982	
R32676	
T47439	
R73968	
H39840	
H95233	
H39841	
N30199	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	

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Figure 4C (Con't)

	201	250
B1KUN10	CGGCACCTGA	ACGGGAGGGG CTCCATTGGG CGTGGCTTTG .AGGGGCTTC
N40851	CGGCACCTGA	ACGGGAGGGG CTCCATTGGG CGTGGCTNTG .AGGGGCTTC
N39876	CGGCACCTGA	ACGGGAGGGG CTCCATTGGG CGTGGCTTTG .AGGGGCTTC
R87894	CGGCACCTGA	ACGGGAGGGG CTCCATTGGG CGTGGCTTTG .AGGGGCTTC
H16866	CGGCACCTGA	ACGGGAGGGG CTCCATTGGG CGTGGCTTTG .AGGGGCTTC
R34808	CGGCACCTGA	ACGGGAGGGG CTCCATTGGG CGTGGCTNTG GAGGGGCTTC
T66038	CGGCACCTGA	ACGGGAGGGG CTCCATTGGG .GTGGCTGTG NAGGGGCTTC
N57450	CGGCACCTGA	ACGGGAGGGG CTCCATTGGG CGTGGCTTTG .AGGGGCTTC
N57374	CGGCACCTGA	ACGGGAGGGG CTCCATTGGG CGTGGCTTNG .AGGGGCTTC
R35464
H94519
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H16757
N27732

CGGCACCTGA

Figure 4C (Con't)

	251		300
B1KUN10	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT GGTGG CGTC GC TG CGCG
N40851	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT GGTGG.CGTC GCCTG.CGCG
N39876	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT GGTGG.CGTC GCCTG.CGCG
R87994	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT GGTNG.CGTC GC.TN.CGCG
H16866	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT GGTNG.CGTC GC.TGCGCG
R34808	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT GGTGGCGCTG GC.TG.CGCG
T66058	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT GGTGG.CGTC GC.TG.CGCG
N57450	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT GGTGG.CGTC GCCTG.CGCG
N57374	CCGGAACCTG	ATCGCGAGAC	CCCAACGGCT GGTGG.CGTC GC.TG.CGCG
R35464
H94519
N39798
H87300
R74593
R31730
R34701
HC2982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

Figure 4C (Con't)

	301		350
Bikunin	TC TCGGCTG	AGCT GGCCA	TGGCGCANT GTTC GGCC T GAGGC GG
N40851	TC TCGGCTG	AGCT GGCCA	TGTCG
N39876	TC TCGGCTG	AGCT GGCCA	TGGCGCACT G TGGCGNGC T GAGGC G
R87894	TC TCGGCTG	AGCTTGGCCA	TGGCGCANT GTTC GGCC T NAGGC GG
H16866	TTCTCGGCTG	AGCT GGCCA	TGGCGCANT GTTC GNGC T GAGGC GG
R34808	TCCTCGGCTG	AGCTGGGCCA	TGGCGCANT GTTC GGCC T GAGGC GG
T66058	TC TCGGCTG	AGCT GGCCA	TGGCGCANT GTTC GNGC T GAGGC GG
N57450	TC TCGGCTG	AGCT GGCCA	TGGCGCANT GGTCC GGCC TTGAGGC GG
N57374	TCCTCGGCTG	AGCT GGCCA	TGGCGCANT GGTCCCGNGC T GAGGCCGG
R35464GGCCGG
H94519
N39798
H87300
R74593
R31730
R34701
H02982
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R73968
H39840
H95233
H39841
N30199
T52966GGCCGG
N29508
N26919
N26910
H16757
N27732

Figure 4C (Con't)

351 400

Bikunin AC GG CG TTTCTCG CC TGCTGGG A TGCTT GC T CCTCTCT
R87894 ACG.

H16866 AC..GCGCT TTTCTTCG. CCTTGCTGGG ATTGGCTTGC TTCTNTCTG
R34808 ACCCGGNCG. TTTTTCGN CCTTGCTGGG ATTG. TG. TTNCTCTCTN
T66058 ...CGGNCG. TTTTCTCG. CC. TGCTGGG A. TGCT. GC T. CCTCTCT.
N57450 ANN. NGCCG. TTTCTCG. CC. TGCTGGG A. TGCT. GC T. CCTCTCT.
N57374 AG. GGCCCG TTTCTCG. CCTTGCTGGG A. TGCT. GC T. CCTCTCTG
R35464GTCT. TTTCTCG. CCTTGCTGGG A. TGCT. GC T. CCTCTCT.
H94519 .GCGCGCG. TTNNTCG. CN. TGCTGGG A. TGCT. GC A. CCTCTCT.
N39798CTGGG ANTGGCT. GC T. CCTCTCT.
H87300
R74593
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N27732

Figure 4C (Con't)

	401		450
B1KUR1A	GGGG TCCTG G	CGGCGGA CCGA GAACG CA GCA TCC	ACGACTT CT
H16866	GGGGTTCCTG	GG.CGGCGGA CCGA.GAACG CA.GCA.TCC	AAGAATTTT
R34808	GGGGTTC.TG	GGGNGCGCGA NCGA.GAACG CAAGCA.TTC	ACGA.TTT
T66058	GGGG.TCCTG	G..CGGCGGA CCGA.GAACG CA.GCA.TCC	ACGANIT.CT
N57450	GGGG.TCCTG	G..CGGCGGA CCGA.GAACG CA.GCA.TCC	ACGACTT.CT
N57374	GGGG.TCCTG	G..CGGCGGA NCGAAGAANG CA.GCAATCC	ANGAATTNCT
R35464	GGGG.TCCTG	G.CGGCGCGA CCGA.GAACG CA.GCA.TCC	ACGACTT.CT
H94519	GGGG.TCGNG	G..CGGCGGA CCGA.GAACG CA.GCA.TCC	ACGACTT.CT
N39798	GGGG.TCCTG	G..CGGCGGA CCGA.GAACG CA.GCA.TCC	ACGACTT.CT
H87300
R74593
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Figure 4C (C n't)

	451	500
9184810	GCCTGGTGT CGAAGGT GG TGGGCAGATG CCGGG CCTC CATGCCTA G	
H16866	GGC	
T66058	TCCTGGTGT CGAAGG	
N57450	GCCTGGTGT. CGAAGGT.GG TGGGCAG	
N57374	GCCTGGTGT CGAAGTTGG TGGGCANATT CCGGGGGCTT CATGNCCTAAG	
R35464	GCCTGGTGT. CGAAGGT.GG TGGGCAGATT CCGGG.CCTC CATGCCTA.G	
H94519	GCCTGGTGT. CGAAGGT.GG TGGGCAGATG CCGGG.CCTC CATGCCTA.G	
N39798	GCCTGGTGT. CGAAGGT.GG TGGGCAGATG CCGGG.CCTC CATGCCTA.G	
H87300	
R74593	
R31730	
R34701	
H02982	
R32676	
T47439	
R73968	
H39840	
H95233	
H39841	
N30199	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	

Figure 4C (Con't)

	501		551
Bikunin	G TGGT GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT ATG		
N57374	GTTCGTGGT ANAATGTNAA TTAANGATTC TTGCAACTGT TTGTGTNATT		
R35464	G.TGGT.GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT.ATG		
H94519	G.TGGT.GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT.ATG		
N39798	G.TGGT.GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT.ATG		
H87300		
R74593		
R31730		
R34701		
H02982		
R32676		
T47439		
R73968		
H39840		
H95233		
H39841		
N30199		
T52966		
N29508		
N26919		
N26910		
H16757		
N27732		

	551		600
Bikunin	GGGGCTGTGA CGGAAACA GCAATAATTA CCTGACCAAG GA GGAGTGC		
N57374	GGGGCTNTTA AACGGAAANA CAATAATNA CCTGACCAAA GAAGNAAT..		
R35464	GGGGCTGTGA ..CGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTGC		
H94519	GGGGCTGTGA ..CGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTGC		
N39798	GGGGCTGTGA ..CGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTGC		
H87300	GATTCGGCAC AGGGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTNC		
R74593 GCAATAATTA CCTGACCAAG GA.GGAGTGC		
R31730		
R34701		
H02982		
R32676		
T47439		
R73968		
H39840		
H95233		
H39841		
N30199		
T52966		
N29508		
N26919		
N26910		
H16757		
N27732		

Figure 4C (C n't)

	601			650
Bikunin	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGCCAC			
R35464	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGCCAC			
H94519	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGCCAC			
N39798	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGCCAC			
H87300	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGCCAC			
R74593	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGCCAC			
R31730			
R34701			
H02982			
R32676			
T47439			
R73968			
H39840			
H95233			
H39841			
N30199			
T52966			
N29508			
N26919			
N26910			
H16757			
N27732			
	651			700
Bikunin	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG			
R35464	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG			
H94519	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG			
N39798	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG			
H87300	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG			
R74593	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG			
R31730			
R34701			
H02982			
R32676			
T47439			
R73968			
H39840			
H95233			
H39841			
N30199			
T52966			
N29508			
N26919			
N26910			
H16757			
N27732			

Figur 4C (Con't)

	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730
Bikunin.	ATTCT GAAG ACCACTCCAG CGATATGTT	CAACTAT	G	AAGAATACTG																										
R35464	ATTCTTGAAG ACCACTTCAG CGATATGTTT	CAANTATTGN	AAGAATAATT																											
H94519	ATTCT.GAAG ACCACTCCAG CGATATGTT.	CAACTAT..G	AAGAATACTG																											
N39798	ATTCT.GAAG ACCACTCCAG CGATATGTT.	CAACTAT..G	AAGAATACTG																											
H8730C	ATTCT.GAAG ACCACTCCAG CGATATGTT.	CAACTAT..G	AAGAATACTG																											
R74593	ATTCT.GAAG ACCACTCCAG CGATATGTT.	CAACTAT..G	AAGAATACTG																											
R31730																											
R34701																											
H02982																											
R32676																											
T47439																											
R73968																											
H3984C																											
H95233																											
H3984:																											
N30199																											
T52966																											
N29508																											
N26919																											
N26910																											
H16757																											
N27732																												

	751	800
Bikunin	CACCGCCAA CGCAGT CAC TGGGCC TTG CCGTG CAT CCTT CCCAC	
R35464	GCACCGNCAA CGNATT	
H94519	GCACCGCCAA CGCATT.CAC TGGGCC..TG C.GTG.CAT. CCTT.CCCAC	
N39798	.CACCGCCAA CGCAGT.CAC TGGGCCCTTG C.GTGGAAAT. CCTTCCGAC	
H87300	.CACCGCCAA CGCAGTNCAC TGGGCC.TTG C.GTGGCAATN CCTT.CCCAC	
R74593	.CACCGCCAA CGCAGT.CAC TGGGCC.TTG CCGTG.CAT. CCTT.CCCAC	
R31730	
R34701	
H02982	
R32676	
T47439	
R73968	
H39840	
495233	
H39841	
N30199	
T52366	
N29508	
N26919	
N26910	
H16757	
N27732	

Figure 4C (Con't)

	801		850
Bikunin	GCTGGTACTT	T GACGTGGA GA GGAAGTC CTG CAATAA	CTTCATCTAT
H94519	GCTGGTACTT	T.GMCGT	
N39798	GCTGGNAATT	INGACGTTGA GAAGGAAC	
H87300	GCTNGTACTT	T.GACGTGGA GA.GGAAGTC CTGGCAATAA	CTTCATCTAT
R74593	GCTGGTACTT	T.GACGTGGA GA.GGAAGTC CTG.CAATAA	CTTCATCTAT
R31730
R34701
H02982	GA GA.GGAAGTC CTG.CAATAA	CTTCATCTAT
R32676	G ATTC..GGAA
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

	851		900
Bikunin	GGAGGCT GC	CGGGGCAAT AAGAACAG C	TACCGCTC T GAGGAGGCT
H87300	GGAGGCTTGC	CGGGGCAATN AAGAACAGNT	TACCGCTCTT TAGGAGGCT
R74593	GGAGGCT.GC	CGGGGCAAT. AAGAACAG.C	TACCGCTC.T GAGGAGGCT
R31730G.C	TACCGCTC.T GAGGAGGCT
R34701
H02982	GGNGGCT.GC	CGGGG.AAT. AAGAACA.NC	TACCGCTC.T GAGGAGGCT
R32676	GGAGGA..GC	CGGGGCAAT. AAGAACAG.C	TACCGCTC.T GAGGAGGCT
T47439NGGCT
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

004413000 111750

[illegible]

	951	1000
Bikunin	GAA TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC	TGG CGGGGG
R74593	GAA TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC	TGGCGGGGGG
R31730	GAA TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC	TGG.CGGGGG
R34701	AAANTCCTCC CCTCCCCCTT GGCTCAAAGG TGGTGGTTC	TGG.CGGGGG
H02982	GAA TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC	TGG.CGGGGG
R32676	GAA TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC	TGG.CGGGGG
T47439	GAA TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC	TGG.CGGGGG
R73968CGGGGG
H39840
H95233
H39841
N30139
T52966
N29508
N26919
N26910
H16757
N27732

Figure 4C (Con't)

	1001	1050
Bikunin	TGTT CGTGA TGGTGTTCAT CC T CTTC TGGG AGCCT CC ATGGTC	
R74593	TGTT CGTGA TGGTGTTCAT CCTT TTC TGGGAGCCT CC ATGGTC	
R31730	TGTT CGTGA TGGTGTTCAT CC T CTTC TGGGAGCCT CC ATGGTC	
R34701	TGTT CGTGA TGGTGTTCAT CCTCTTTC GGG AGCCT CCTATGGTC	
H02982	TGTT CGTGA TGGTGTTCAT CC T CTTC TGGG AGCCT CC ATGGTN	
R32676	TGTT CGTGA TGGTGTTCAT CC T CTTC TGGG AGCCT CC ATGGTC	
T47439	TGTT CGTGA TGGTGTTCAT CC T CTTC TGGG AGCCT CC ATGGTC	
R73968	TGTT CGTGA TGGTGTTCAT CC T CTTC TGGG AGCCT CC ATGGTC	
R39840	
H95233	
H39841	
N30199	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	

	1051		1100
B1KUN18	TACC TGAT	CCGGGTGGCA	CGGAGG AAC C AGG AGCG TGCCCTGGCC
R74593	TAC...TGATT	CCGGGTGGCA	AGGAGG AAC C AGG AGCG TGCCCTGGCC
R31730	TACC TGAT	CCGGGTGGCA	CGGAGGGAAC C AGGGAGCG TGCCCTGGCC
R34701	TACCCTGAT	CCGGGTGGCA	CGGAGG AAC CCAGG ANCG TGCCCTGGCC
H02982	TACC TGAT	CCGGGTNGCA	CGGAGG AAC C AGGGAGCG TGCCCTGGCN
R32676	TACC TGAT	CCGGGTGGCA	CGGAGG AAC C AGGGAGCG TGCCCTGGCC
T47439	TACC TGAT	CCGGGTNGCA	CGGAGG AAC C AGG AGCG TGCCCTGGCC
R73968	TACC TGAT	CCGGGTGGCA	CGGAGG AAC C AGG AGCG TGCCCTGGCC
H39840GGG AAC	C AGG AGCG TGCCCTGGCC
H95233
H39841
N30199GAGGAACC	C ANG AGCT TGCCCTGGCC
T52966
N29508
N26919
N26910
H16757
N27732

Figure 4C (Con't)

1101 1150

Bikunin ACCG TCT G GAGCTCCGGA GATGACAAGG AGCAGCTGG TGAAGAAC
 R74593 ANCG.TCT.G GAGCTTCGGA GATGACAAGG GNT
 R31730 ACCG.TCTGG GAGCTCCGGA GATGACAAGG GAGCAGCTGG GTGAAGAAC.
 R34701 ACCG.TCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.
 H02982 ACCG.TCTNG GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.
 R32676 ACCG.TCTGG GAGCTCCGGA GATGACAAGG GAGCAGCTGG .TGAAGAAC.
 T47439 ACCG.TCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.
 R73968 ACCG.TCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.
 H39840 ACCGGTCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.
 H95233
 H39841
 N30199 ACCG.TCT.G GAGCTCCGGA GATNACAANG .AGCAGCTGN .TGAAGAACC
 T52966
 N29508
 N26919
 N26910
 H16757
 N27732

1151 1200

Bikunin ACATATGT C CTGT GACCG CCTGT CGC C AAGAGG A CT GGGGAA
 R31730 ACATATGTTT CTGTTGACCG NCCTGTTCCG C.AAGAGG.A TTGGGGGAA.
 R34701 ACATATGT.C CTGT.GACCG CCTGT.CGC C.AAGAGG.A CT.GGGGAA.
 H02982 ACATATGT.C CTGT.GACCG NCCTGTTCCG C.AAGAGG.A CTNGGGGAAA
 R32676 ACATATGTTT CTGTTGACCG CCTGTTCCG C.AAGAGGGA NTGGGGGAA.
 T47439 ACATATGT.C CTGT.GACCG CCTGT.CGC C.AAGAGG.A CT.GGGGAA.
 R73968 ACATATGT.C CTGT.GACCG CCTGT.CGC C.AAGAGG.A CT.GGGGAA.
 H39840 ACATATGT.C CTGT.GACCG CCTGT.CGC C.AAGAGG.A CT.GGGGAA.
 H95233
 H39841C. CCTGT.CGC CAAAAGG.A CT.GGGGAA.
 N30199 ACATATGT.C CTGT.GACCG CCTNT.CGC C.AAGAGG.A CT.GGGNAAA
 T52966
 N29508C. CCTNT.CGC C.AAGAGG.A CT.GGC.AA.
 N26919
 N26910
 H16757
 N27732

Figure 4C (Con't)

1201 1250

Bikunin GGGAGGGG AGACTAT G TGT GA GCT TTTTTT AA A TAGA GG
 R31730 .GGGAGGGG A
 R34701 .GGGAGGGG. AGACTAT.G. TGT.GA.GCT TTTTTT..AA A.TA
 H02982 GGGAGGGG. AGATTAT.G. TGTGA.GTT TTTTTT..AA ANTAG
 R32676 GGGAGGGG AGANTATTGT TGTGA.GNT TTTTTTAAA ATTAGAGGG
 T47439 .GGGAGGGG. AGACTAT.G. TGT.GA.GCT TTTTTT..AA A.TAGA..GG
 R73968 .GGGAGGGG. AGACTAT.G. TGT.GA.GCT TTTTTT..AA A.TAGA..GG
 H39840 .GGGAGGGG. AGACTAT.G. TGT.GA.GCT TTTTTT..AA A.TAGA..GG
 H95233
 H39841 .GGGAGGGG AAACNAT.G. TGT.GAACCT TTTTTT.AAA A.TAGA..GG
 N30199 .GGGAGGGG. AGACTAT.G. TGT.AA.GCT TTTTTT..AA A.TAGA..GG
 T52966
 N29508 .GGGAGGGG. AGACTA..G. TGT.GA.GCT TTTTTT..AA A.TAGA..GG
 N26919
 N26910
 H16757
 N27732

1251 1300

Bikunin GATTGACTC GGATTTC A GT GATC A TTAGGG CT GAGGTCTGTT
 R32676 GNTTGANTTC GGGNTTTTNA GTTGATCCAT TTAGGGGGNT GAG
 T47439 GATTGACTC..GGATTTC.A GT.GATC.A. TTAGGG..CT GAGGTCTNTT
 R73968 GATTGACTC..GGATTTC.A GT.GATC.A. TTAGGG..CT GAGGTCTGTT
 H39840 GATTGACTC..GGATTTC.A GT.GATC.A. TTAGGG..CT GAGGTCTGTT
 H95233A. TTAGGG..CT GAGGTCTGTT
 H39841 GATTGACTC..GGATTTC.A GT.GATC.A. TTAGGG..CT GAGGTCTGTT
 N30199 GATTGACTC..GGATTTCGA GT.GATC.A. TTAGGG..CT GAGGTCTGTT
 T52966
 N29508 GATTGACTC..GGATTTC.A GT.GATCNA. TTAGGG..CT GAGGTCTGTT
 N26919
 N26910
 H16757
 N27732

1301 1350

Bikunin TCTCTGGGAG GTAGGACGGC TGGTTTC TG G TC TGGCA GGGATGGG
 T47439 TCTCTNGGAG GTAGGACGA
 R73968 TCTCTGGGAG GTAGGACGGC TGGTTTC TG GGTCTTGGCA GGGATGGG
 H39840 TCTCTGGGAG GTAGGACGGC TGGTTTC TG G.TC.TGGCA GGGATGGG
 H95233 NCTCTGGGAG NTAGGACGGC TGGTTTC TG G.TC.TGGCA GGGATGGG
 H39841 TCNCTGGGAG GTAGGACGGC TGGTTTC TG G.TC.TGGCA GGGATGGG
 N30199 TCTCTGGGAG GTAGGACGGC TGGTTTC TG G.TC.TGGCA GGGATGGG
 T52966G.TC.TGGCA GGGATGGG
 N29508 TCTCTGGGAG GTAGGACGGC TGGTTTC TG G.TC.TGGCA GGGATGGG
 N26919
 N26910
 H16757G.TC.TGGCA GGGATGGG
 N27732GGCTG GGTCTCTGCA AGGNATGGG

: 351

: 400

1450

: SOC

Figure 4C (Con't)

1501 1550
 Bikunin CTCTTTT CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT GT
 H39840 CTCTTTT CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTTGT
 H95233 CTCTTTT CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT GT
 H39841 CTCTTTT CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT GT
 N30199 CTCTTTT CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT GT
 T52966 CTCTTTT CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT GT
 N29508 CTCTTTT CT CATCACAGAA GTGATGTTG AATCGTTTCT TTTGTTT GT
 N26919 CTCTTTT CN CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT GT
 N26910 CTCTTTT CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT GT
 H16757 CTCTTTTACT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT GT
 N27732 CTCTTTT CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT GT

1551 1600
 Bikunin CTGATTTATG G TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 H39840 CTGATTTATG GGTTTTTT AAGTAT
 H95233 CTGATTTATG G..TTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 H39841 CTGATTTATG G..TTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 N30199 CTGATTTATG G..TTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 T52966 CTGATTTATG G..TTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 N29508 CTGATTTATG G..TTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 N26919 CTGATTTATG G..TTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 N26910 CTGATTTATG G..TTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 H16757 CTGATTTATG G..TTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 N27732 CTGATTTATG G..TTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT

1601 1650
 Bikunin CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
 H95233 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAA
 H39841 CTGAAAGAAG GAAAGTAAAN TGTACAAGTT TAATAAAAAG GGGCCTTCCC
 N30199 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
 T52966 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
 N29508 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
 N26919 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
 N26910 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
 H16757 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
 N27732 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC

1651 1689
 Bikunin CTTTAG AAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
 H39841 CTTTAA.
 N30199 CTTTAG.AAT AAA
 T52966 CTTTAGGAAT NAAAAA AAAAGGTC
 N29508 CTTTAG.AAT AAATTTCAGC ATGTGCTTTC AA
 N26919 CTTTAG.AAT AAAAAAAAAA AAAAAAAAAA A
 N26910 CTTTAG.AAT AAATTTCAGC ATGTGCTTTC AAAAAA
 H16757 CTTTAG.AAT AAAAAAAAAA AAAAAAAAAA AAAAAA
 N27732 CTTTAG.AAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

FIGURE 4D

27

EST consens MLRAEADGVS RLLGSLLLSG VLAADRERSI HDFCLVSKVV GRCRASHPRW 50
EST consens WYNVTDGSCQ LFVYGGCDGN SMNYLTKEEC LKKCATVTEN ATGDLATSRN 100
EST consens AADSSVPSAP RRQDSEDHSS DMFNYEEYCT ANAVTGPCRA SFPRWYFDVE 150
EST consens RNSCNFIYG GCRGNKNSYR SEEACMLRCF RQENPPLPL GSKYVYLAGL 200
EST consens FVMVLLIFLG ASMYXLRVA RRNQERALRT VWSGGDDKEQ LVKNITYVL 248

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FIGURE 4E

28

cDNA ACC 3
 translation T -47

cDNA TGATCGCGAG ACCCCAACGG CTGGTGGCGT CGCCTGCGCG TCTCGGCTGA 53
 translation S R D P N G W W R R L R V S A E -30

cDNA GCTGGCCATG GCGCAGCTGT GCGGGCTGAG GCGGAGCCGG GCGTTTCTCG 103
 translation L A M A Q L C G L R R S R A F L A-13

cDNA CCCTGCTGGG ATCGCTGCTC CTCTCTGGGG TCCTGGCJGC CGACCGAGAA 153
 translation L L G S L L L S G V L A A D R E 4

cDNA CGCAGCATCC ACGACTTCTG CCTGGTGTCTG AAGGTGGTGG GCAGATGCCG 203
 translation R S I H D F C L V S K V V G R C R 21

cDNA GGCTCCATG CCTAGGTGGT GGTACAATGT CACTGACGGA TCCTGCCAGC 253
 translation A S M P R W W Y N V T D G S C Q L 38

cDNA TGTTTGTGTA TGGGGGCTGT GACGGAACA GCAATAATTA CCTGACCAAG 303
 translation F V Y G G C D G N S N N Y L T K 54

cDNA GAGGAGTGCC TCAAGAAATG TGCCACTGTC ACAGAGAATG CCACGGGTGA 353
 translation E E C L K K C A T V T E N A T G D 71

cDNA CCTGGCCACC AGCAGGAATG CAGCGGATTC CTCTGTCCCA AGTGCTCCCA 403
 translation L A T S R N A A D S S V P S A P R 88

cDNA GAAGGCAGGA TTCTGAAGAC CACTCCAGCG ATATGTTCAA CTATGAAGAA 453
 translation R Q D S E D H S S D M F N Y E E 104

cDNA TACTGCACCG CCAACGCAGT CACTGGGCCT TGCCGTGCAT CCTCCCACG 503
 translation Y C T A N A V T G P C R A S F P R 121

cDNA CTGGTACTTT GACGTGGAGA GGAACCTCTG CAATAACTTC ATCTATGGAG 553
 translation W Y F D V E R N S C N N F I Y G G 138

cDNA GCTGCCGGGG CAATAAGAAC AGCTACCGCT CTGAGGAGGC CTGCATGCTC 603
 translation C R G N K N S Y R S E E A C H L 154

cDNA CGCTGCTTCC GCCAGCAGGA GAATCCTCCC CTGCCCCTTG GCTCAAAGGT 653
 translation R C F R Q Q E N P P L P L G S K Y 171

cDNA GGTGGTTCTG GCGGGGCTGT TCGTGATGGT GTTGATCCTC TTCCTGGGAG 703
 translation V V L A G L F Y M V L L L F L G A 193

cDNA CCTCCATGGT CTACCTGATC CGGGTGGCAC GGAGGAACCA GGAGCGTGCC 753
 translation S M V Y L R V A R R N Q E R A 204

cDNA CTGCGCACCG TCTGGAGCTT CGGAGATGA 732
 translation L R T V W S F G D 213

FIGURE 4F

29

cDNA GCACGAGTTG GGAGGTGTAG CGCGGCTCTG AACGCGCTGA GGGCCGTTGA 50
 cDNA GTGTGCGAGG CGGCGAGGGC GCGAGTGAGG AGCAGACCCA GGCATCGCGC 100
 cDNA GCGGAGAAGG CCGGGCGTCC CCACACTGAA GGTCCGAAAA GCGGACTTCC 150
 cDNA GGGGGCTTTG GCACCTGGCG GACCCCTCCCG GAGCGTCGGC ACCTGAACGC 200
 cDNA GAGGCGCTCC ATTGCGCGTG CGCGTTGAGG GGCTTCCCGC ACCTGATCGC 250
 cDNA GAGACCCCAA CGGCTGGTGG CGTCGCCTGC GCGTCTCGGC TGAGCTGGCC 300
 cDNA ATGGCGCAGC TGTGCGGGCT GAGGCGGAGC CGGGCGTTTC TCGCCCTGCT 350
 translation M A Q L C G L R R S R A F L A L L -11

cDNA GGGATCGCTG CTCCTCTCTG GGGTCCTGGC GGCCGACCGA GAACGCAGCA 400
 translation G S L L L S G V L A A D R E R S I -

cDNA TCCACGACTT CTGCCTGGTG TCGAAGGTGG TGGGCAGATG CCGGGCCTCC 450
 translation H D F C L V S K V V G R C R A S 23

cDNA ATGCCTAGGT GGTGGTACAA TGTCAC TGACCTGCC AGCTGTTTGT 500
 translation M P R W W Y N V T D G S C Q L F V 40

cDNA GTATGGGGGC TGTGACGGAA ACAGCAATAA TTACCTGACC AAGGAGGAGT 550
 translation Y G G C D G N S N N Y L T K E E C 57

cDNA GCCTCAAGAA ATGTGCCACT GTCACAGAGA ATGCCACGGG TGACCTGGCC 600
 translation L K K C A T V T E N A T G D L A 73

cDNA ACCAGCAGGA ATGCAGCGGA TTCCTCTGTC CCAAGTGCTC CCAGAAGGCA 650
 translation T S R N A A D S S V P S A P R R Q 90

cDNA GGATTCTGAA GACCACTCCA GCGATATGTT CAACTATGAA GAATACTGCA 700
 translation D S E D H S S D M F N Y E E Y C T 107

cDNA CCGCCAACGC AGTCACTGGG CTTTGCCGTG CATCCTTCCC ACGCTGGTAC 750
 translation A N A V T G P C R A S F P R W Y 123

cDNA TTTGACGTGG AGAGGAACTC CTGCAATAAC TTCATCTATG GAGGCTGCCG 800
 translation F D V E R N S C N N F I Y G G C R 140

cDNA GGGCAATAAG AACAGCTACC GCTCTGAGGA GGCCTGCATG CTCGCTGCT 850
 translation G N K N S Y R S E E A C M L R C F 157

cDNA TCCGCCAGCA GGAGAATCCT CCCCTGCCCC TTGGCTCAAA GGTGGTGGTT 900
 translation R Q Q E N P P L P L G S K V V V 173

cDNA CTGGCGGGGC TGTTCGTGAT GGTGTTGATC CTCTTCTGG GAGCCTCCAT 950
 translation L A G L F V M Y L L L F L G A S M 190

cDNA GGTCTACCTG ATCCGGGTGG CACGGAGGAA CCAGGAGCGT GCCCTGCGCA 1000
 translation V Y L R V A R R N Q E R A L R T 207

cDNA CCGTCTGGAG CTCGGGAGAT GACAAGGAGC AGCTGGTGAA GAACACATAT 1050
 translation V W S S G D D K E Q L V K N T Y 223

cDNA GTCCTGTGAC CGCCCTGTGG CCAAGAGGAC TGGGGAAGGG AGGGGAGACT 1100
 translation V L * 225

30

cDNA	ATGTGTGAGC	TTTTTTTAA	TAGAGGGATT	GACTCGGATT	TGAGTGATCA	1150
cDNA	TTAGGGCTGA	GGTCTGTTTC	TCTGGGAGGT	AGGACGGCTG	CTTCCTGGTC	1200
cDNA	TGGCAGGGAT	GGGTTTGCTT	TGGAAATCCT	CTAGGAGGCT	CCTCCTCGCA	1250
cDNA	TGGCCTGCAG	TCTGGCAGCA	GCCCCGAGTT	GTTTCCTCGC	TGATCGATTT	1300
cDNA	CTTTCCTCCA	GGTAGAGTTT	TCTTTGCTTA	TGTTGAATTC	CATTGCCTCC	1350
cDNA	TTTTCTCNAT	CACAGAAGTG	ATGTTGGAAT	CGTTTCTTTT	GTTTGTCCTGA	1400
cDNA	TTTATGGTTT	TTTTAAGTAT	AAACAAAAGT	TTTTTATTAG	CATTCTGAAA	1450
cDNA	GAAGGAAAGT	AAAATGTACA	AGTTTAAATA	AAAGGGGCCCT	TCCCCCTTAG	1500
cDNA	AATAAATTTC	CAGCATGTTG	CTTTCAAAAA	AAAAAAAAAA	AAAA	

[illegible]

FIGURE 4G

31

EST consens			MLR	AADGVSRLL	GSLLLSGVLA	-2
PCR clone			MAQLCGL	RRSRAFLALL	GSLLLSGVLA	-1
λcDNA clon			MAQLCGL	RRSRAFLALL	GSLLLSGVLA	-1
EST consens	ADERSIHDF	CLVSKVVGR	RASMPRWYN	VTDGSCQLFV	YGGCDGNSNN	50
PCR clone	ADERSIHDF	CLVSKVVGR	RASMPRWYN	VTDGSCQLFV	YGGCDGNSNN	50
λcDNA clone	ADERSIHDF	CLVSKVVGR	RASMPRWYN	VTDGSCQLFV	YGGCDGNSNN	50
EST consens	YLTKEECLKK	CATVTENATG	DLATSRNAAD	SSVPSAFRRQ	DSEDHSSDMF	100
PCR clone	YLTKEECLKK	CATVTENATG	DLATSRNAAD	SSVPSAFRRQ	DSEDHSSDMF	100
λcDNA clone	YLTKEECLKK	CATVTENATG	DLATSRNAAD	SSVPSAFRRQ	DSEDHSSDMF	100
EST consens	NYEEYCTANA	VTGPCRASFP	RWYFDVERNS	CNNFIYGGCR	GNKNYSRSEE	150
PCR clone	NYEEYCTANA	VTGPCRASFP	RWYFDVERNS	CNNFIYGGCR	GNKNYSRSEE	150
λcDNA clone	NYEEYCTANA	VTGPCRASFP	RWYFDVERNS	CNNFIYGGCR	GNKNYSRSEE	150
EST consens	ACMLRCFRQQ	ENPPLPLGSK	<u>VVYLAGLEVY</u>	<u>VLLIFLGASH</u>	<u>VYLRVARRN</u>	200
PCR clone	ACMLRCFRQQ	ENPPLPLGSK	<u>VVYLAGLEVY</u>	<u>VLLIFLGASH</u>	<u>VYLRVARRN</u>	200
λcDNA clone	ACMLRCFRQQ	ENPPLPLGSK	<u>VVYLAGLEVY</u>	<u>VLLIFLGASH</u>	<u>VYLRVARRN</u>	200
EST consens	QERALRTVWS	SGDDKEQLVK	NTYVL			225
PCR clone	QERALRTVWS	FGD				213
λcDNA clone	QERALRTVWS	SGDDKEQLVK	NTYVL			225

Purification of Placental Bikunin using Superdex 75 Gel-Filtration

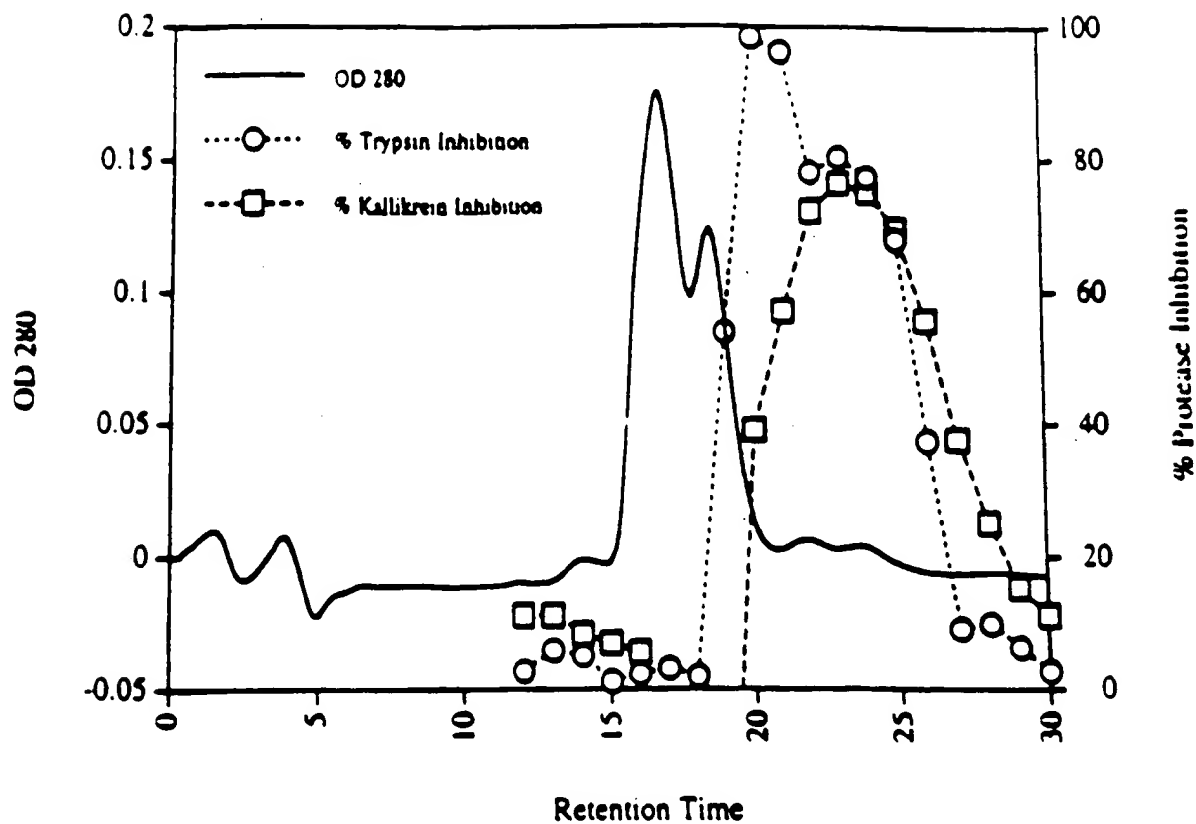


FIGURE 5

OD 215

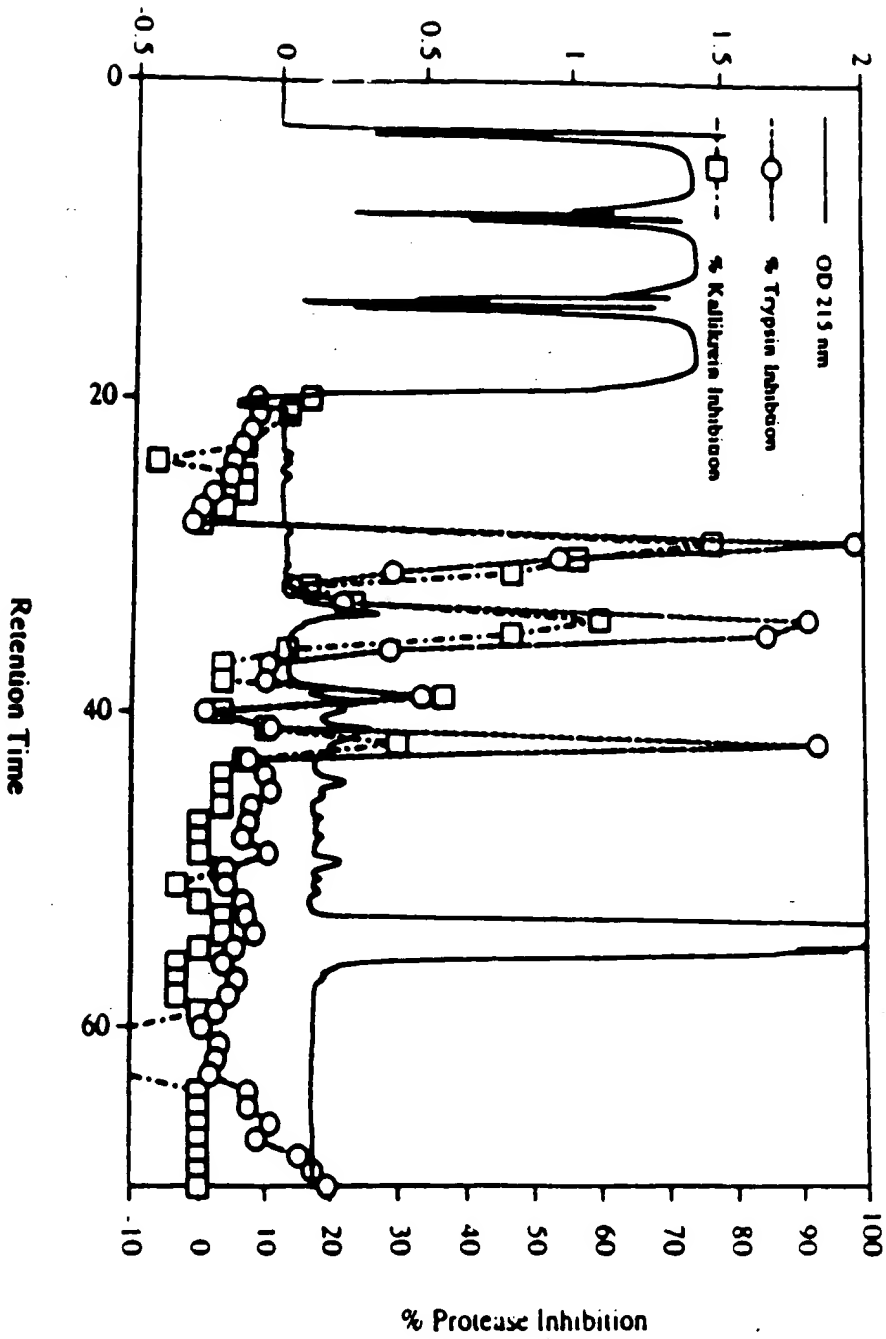


FIGURE 6

Purification of Placental Bikunin using C18 Reverse-Phase Chromatography

Figure 7

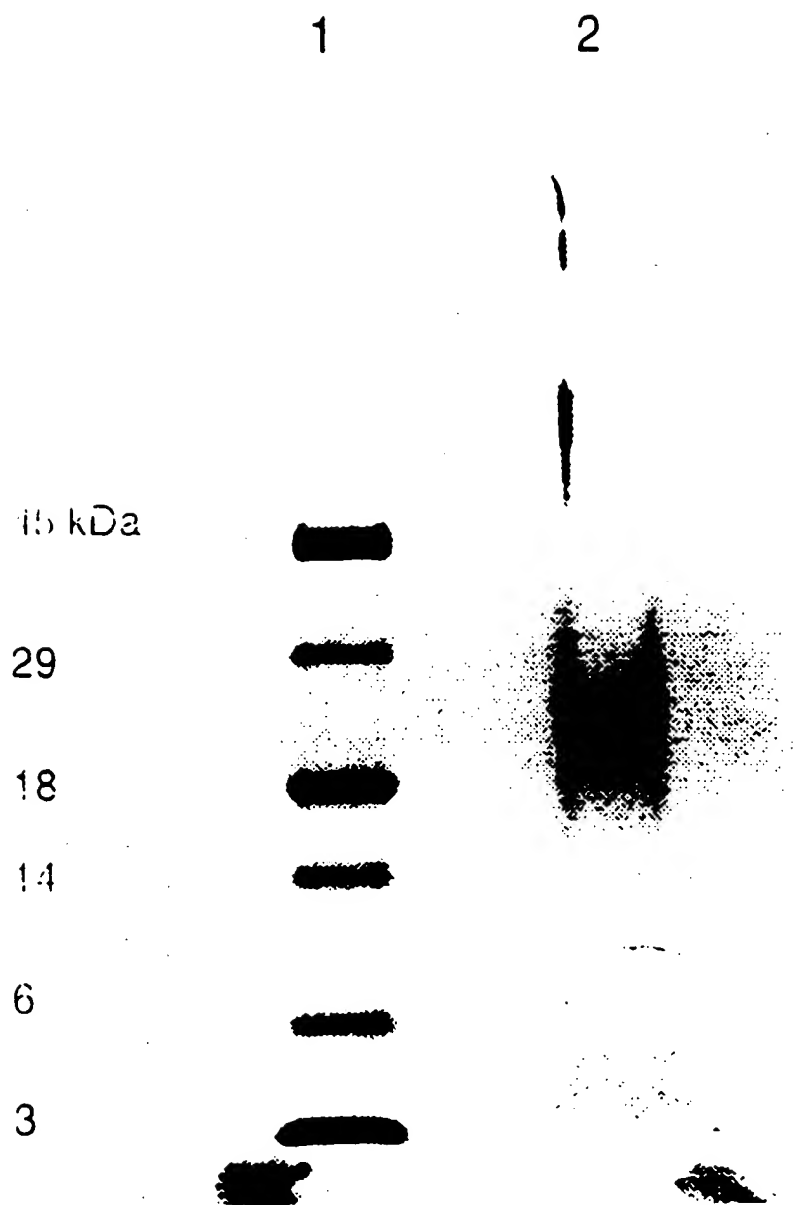


Figure 8A

35

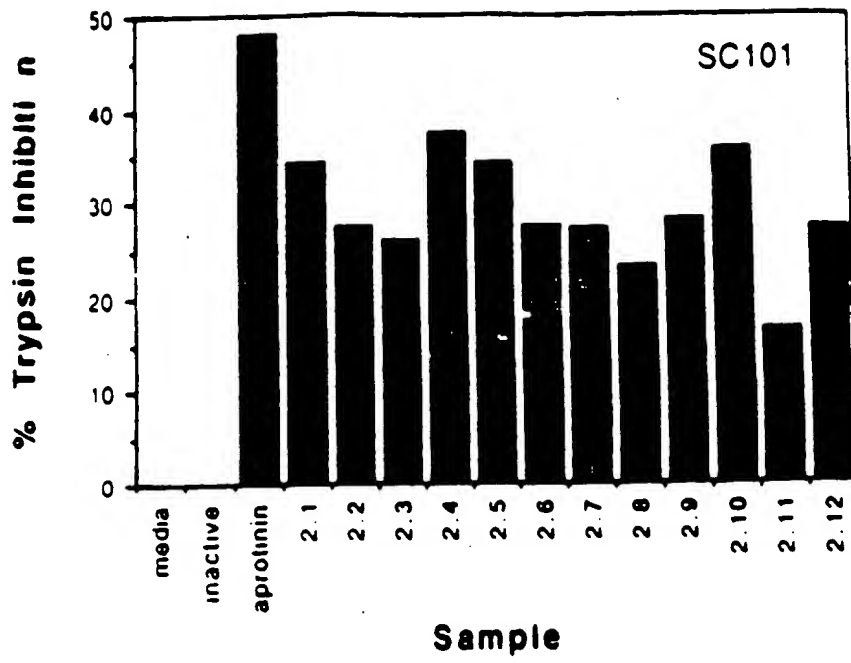


Figure 8B

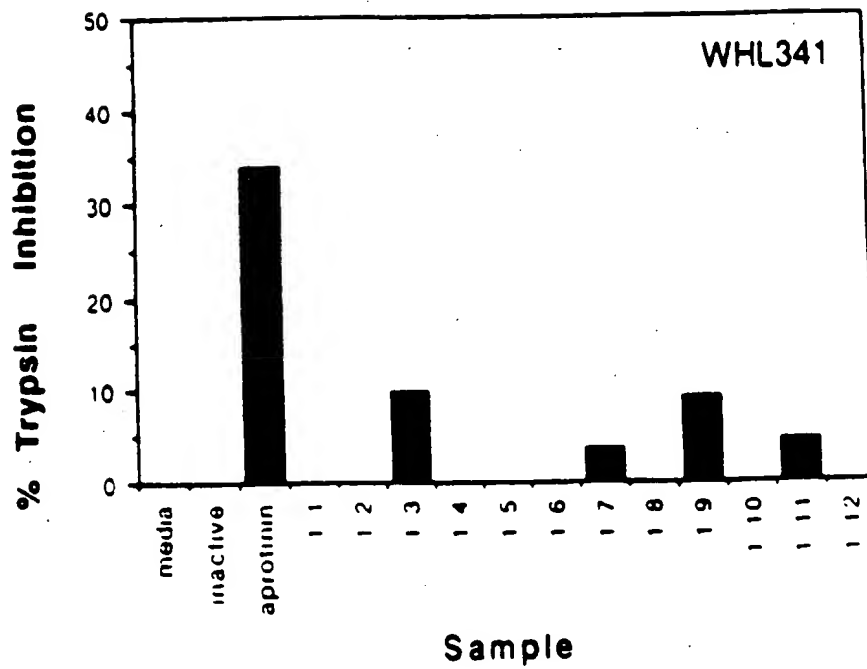


Figure 9A

SDS-PAGE

Aprotinin
2.4
2.5

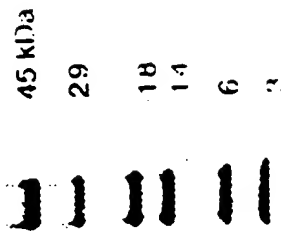


Figure 9B

Western

Aprotinin
2.4
2.5

45 kDa
29
18
14
6
3

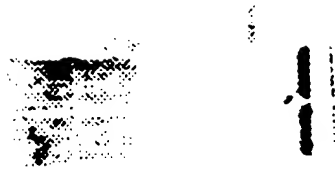


Figure 10

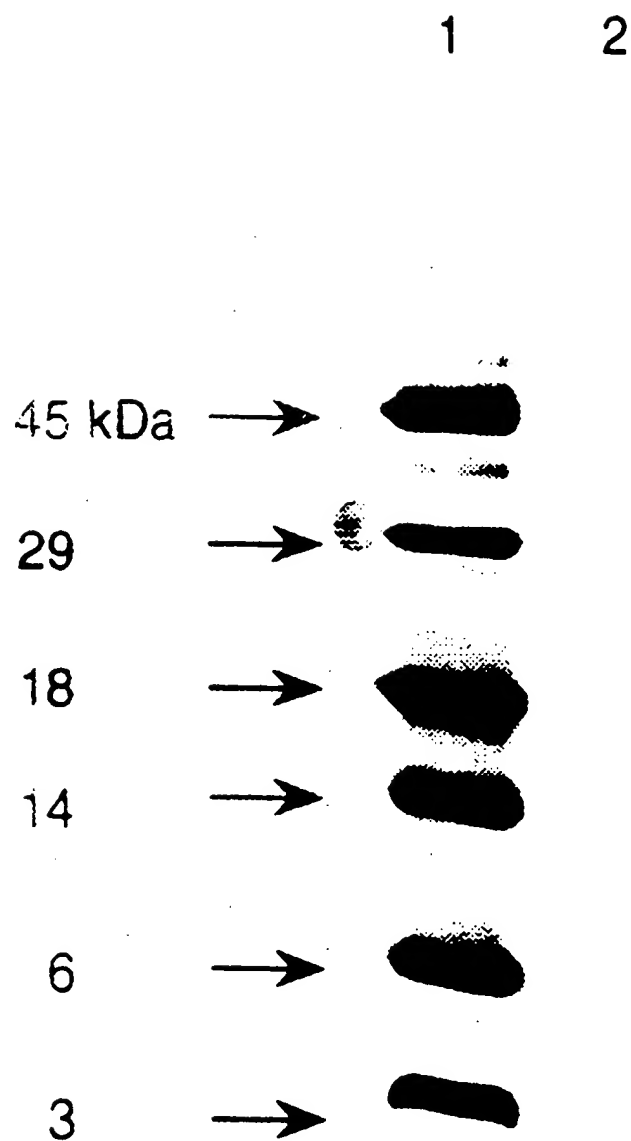


Figure 11A

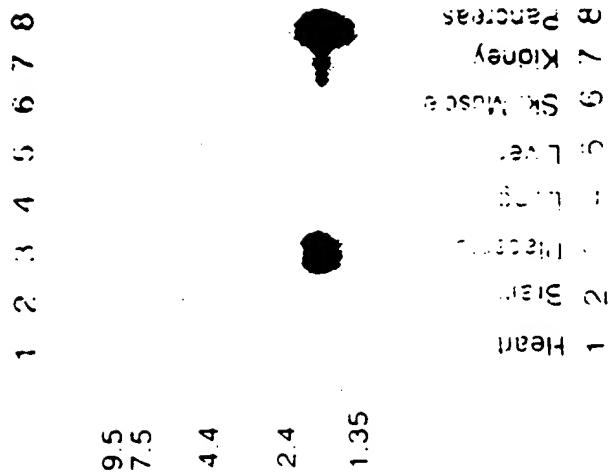


Figure 11B

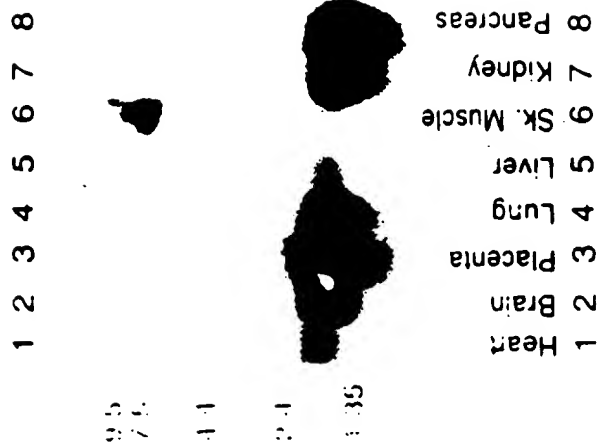


Figure 12A

1 2 3 4

45 kDa
29
18
14
6
3

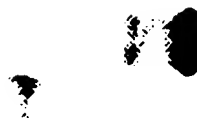


Figure 12B

1 2 3 4

45 kDa
29
18
14
6
3



Figure 13

1 2

45 kDa

29

18

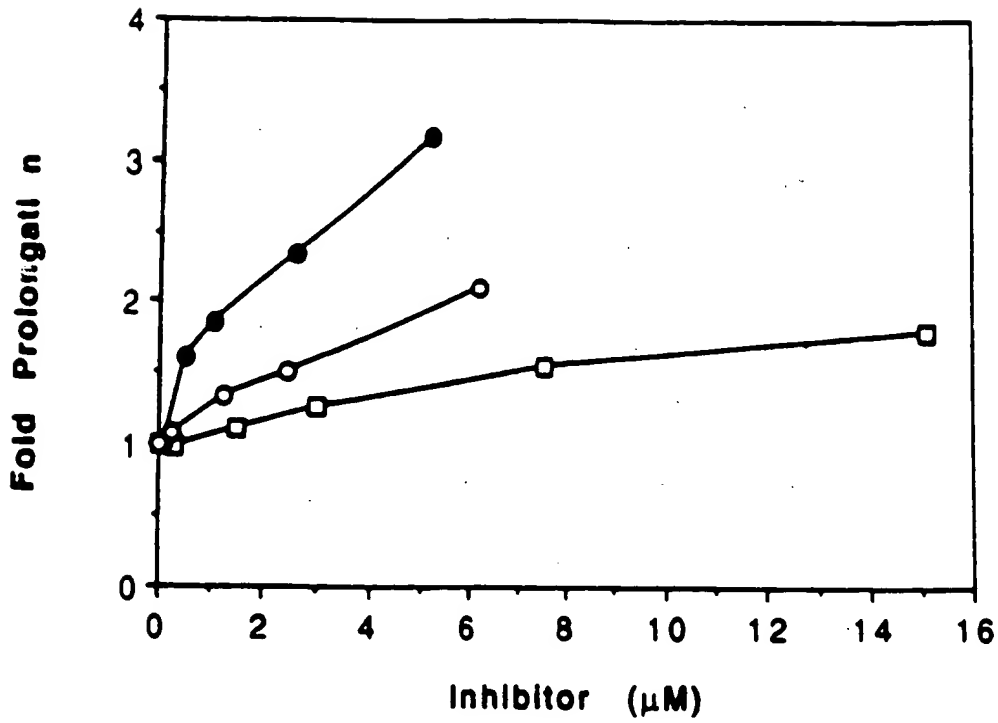
14

6

3



Figure 14



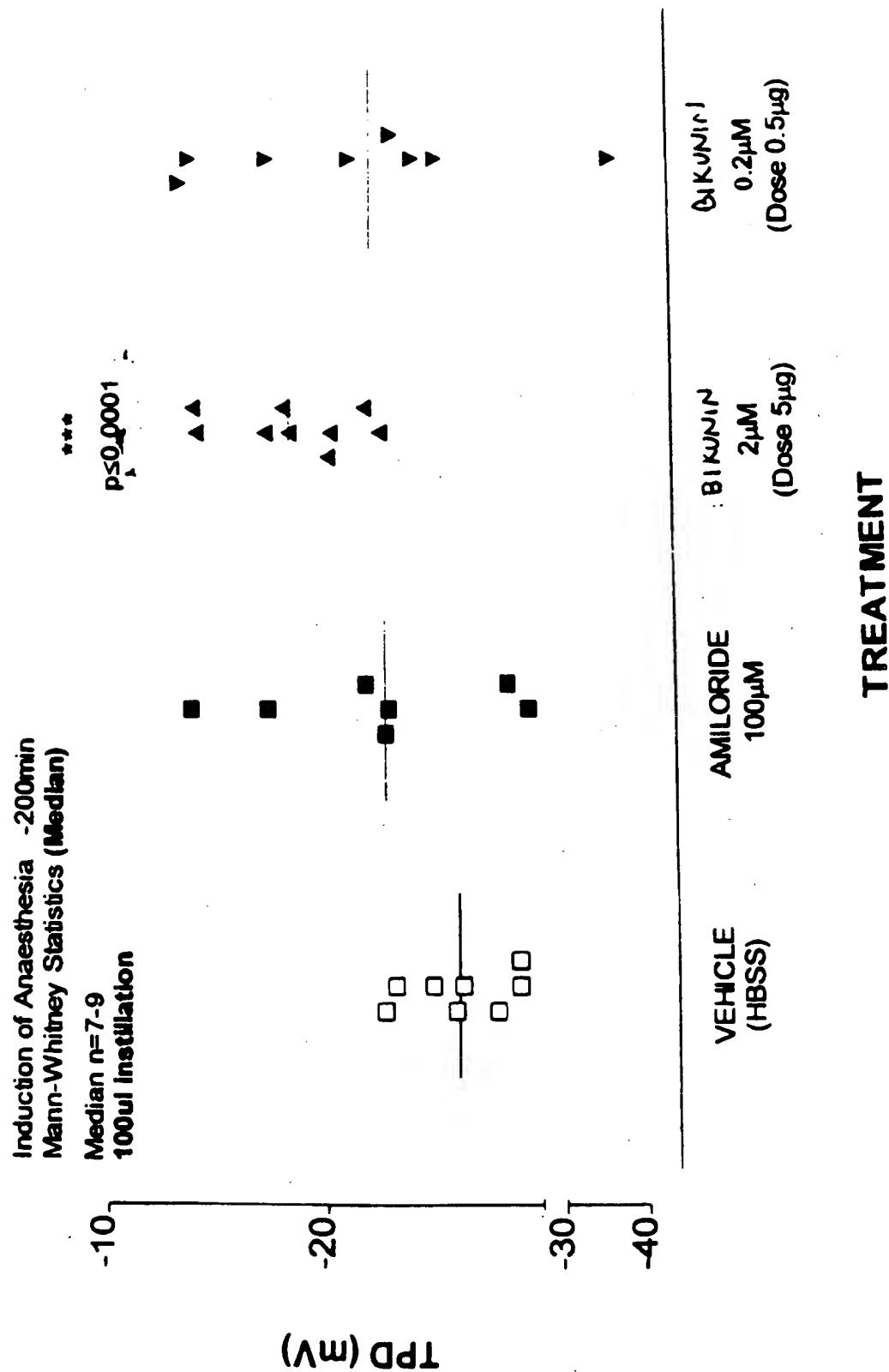
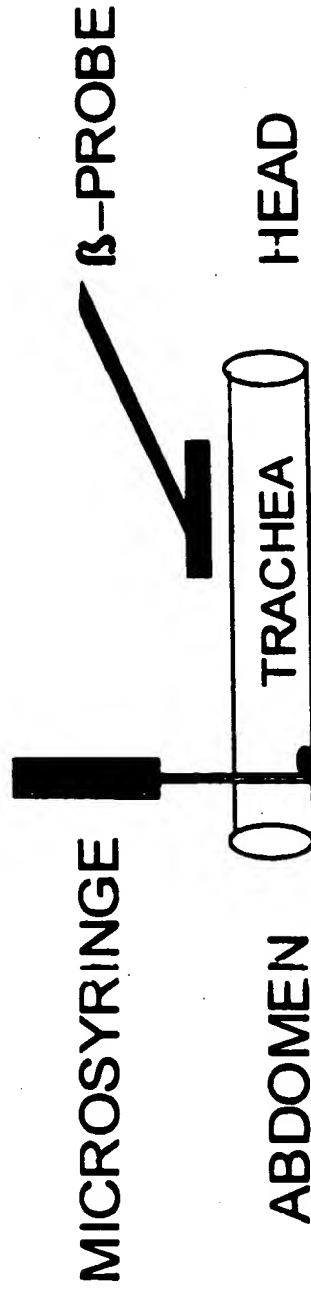
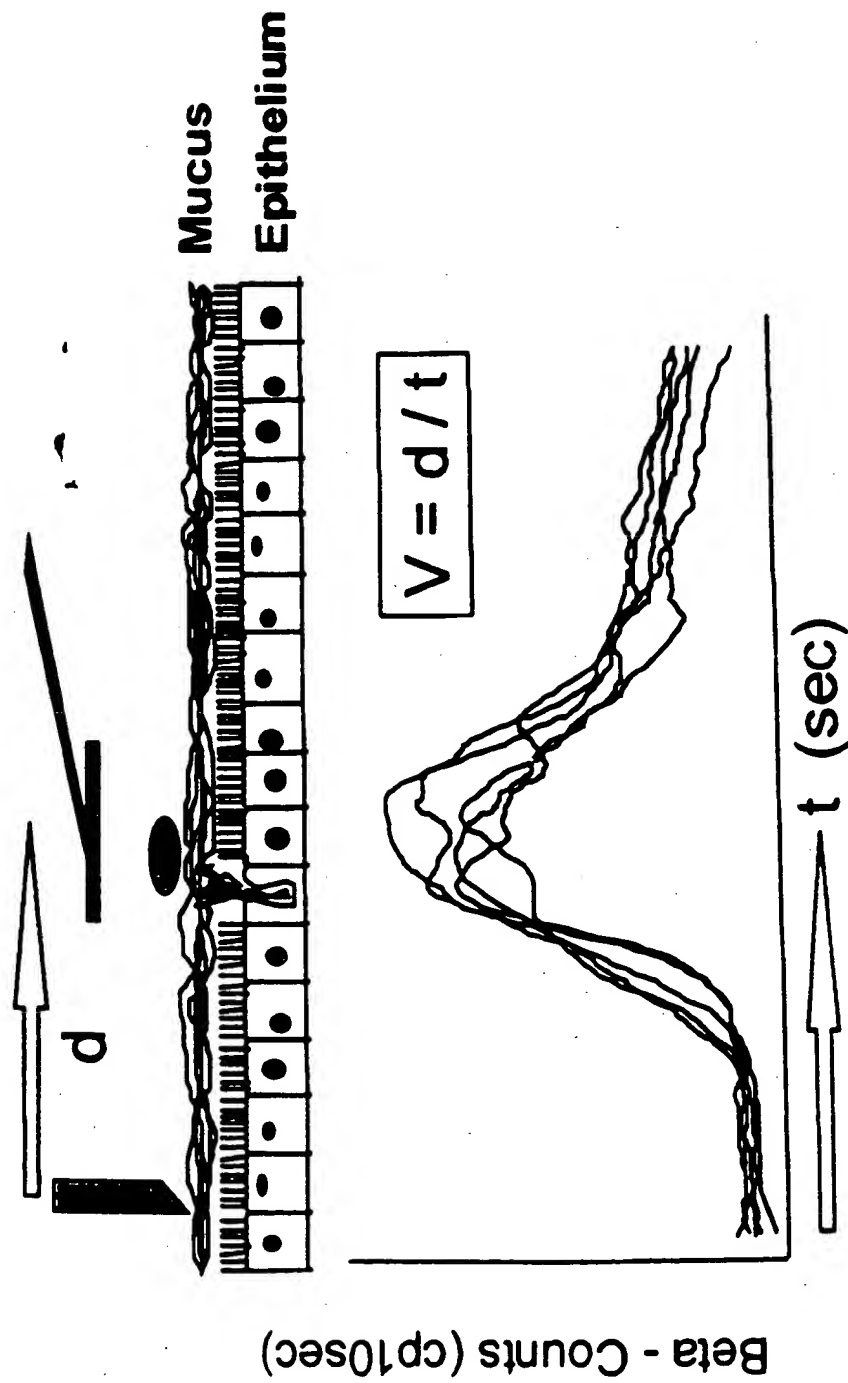


Figure 16 (a) : Diagram to show the arrangement of needle and Beta probe.



Longitudinal view

Figure 16 (b) : Counts detected by the probe as the ^{32}P -labeled Saccharomyces cerevisiae are transported along the tracheal mucociliary layer.



Sustained Increase in Tracheal Mucus Velocity In Vivo in Guinea Pig in Response to Bikunin

Figure 16(c)

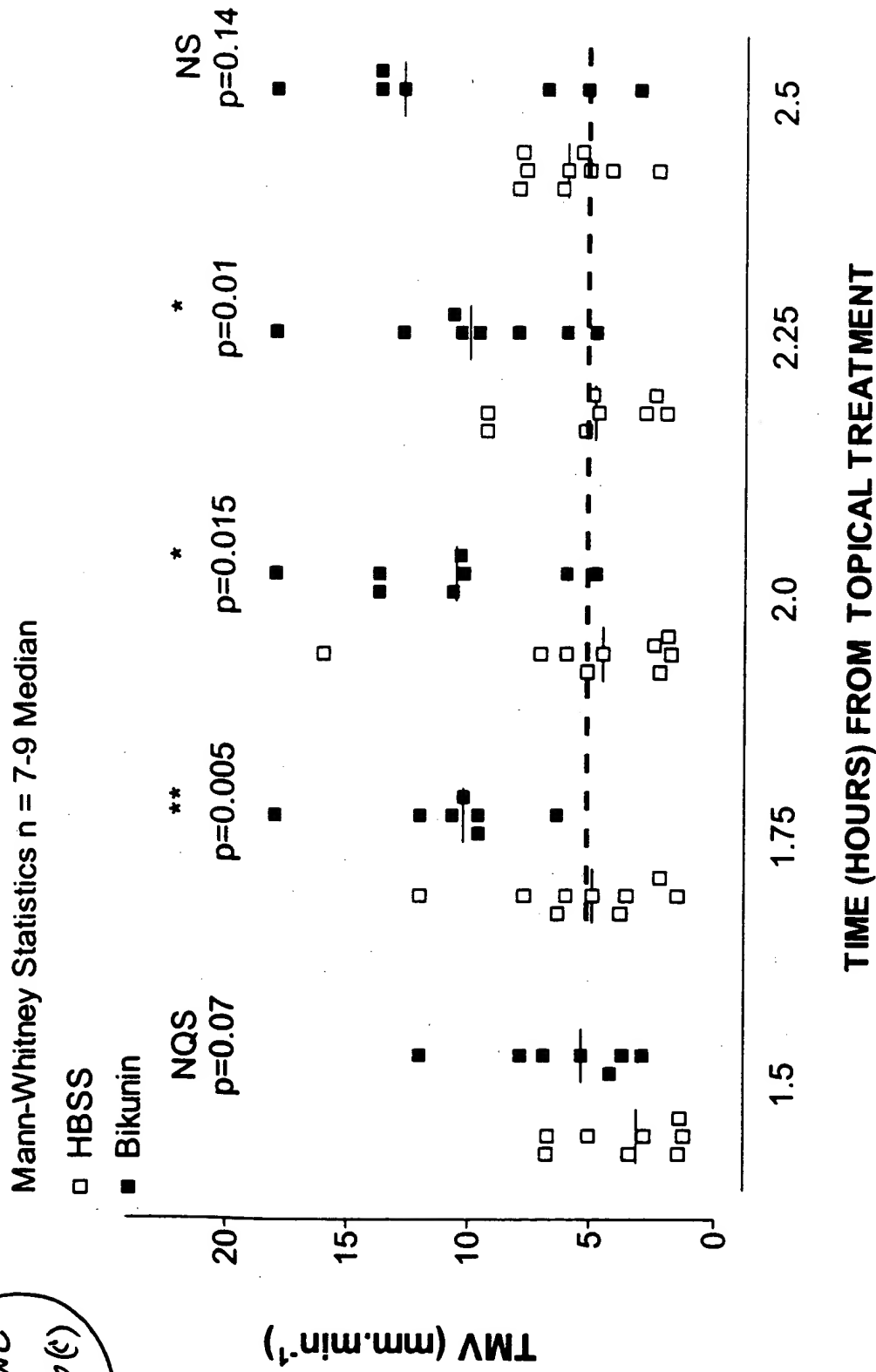


Figure 17 : Short circuit current (Isc) trace to show the action of β IKUNIN (70nM) on sodium dependent current in cultured normal human bronchial epithelial cells in vitro

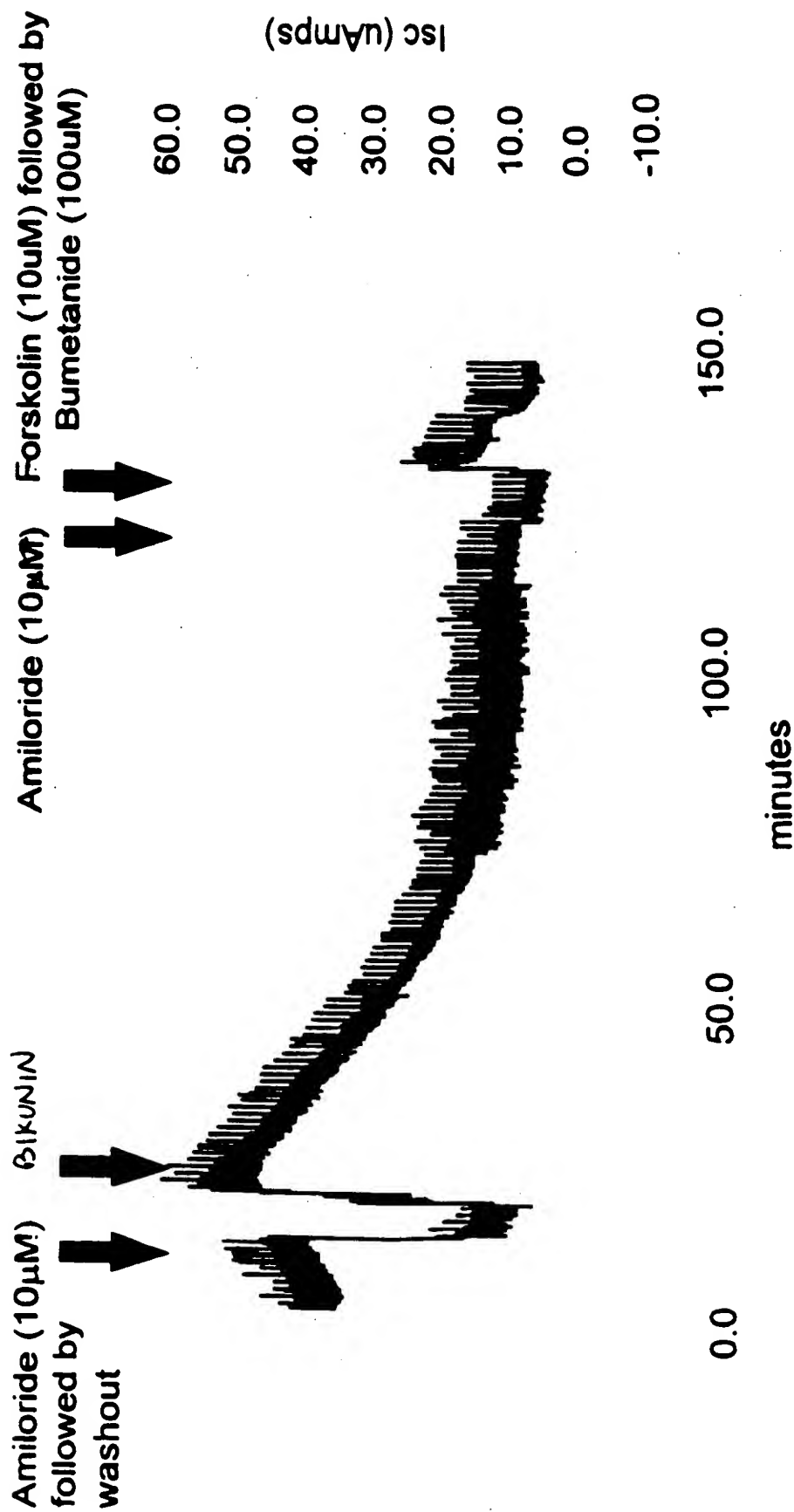


Figure 18 : The effect of a 5 min aerosol of hypertonic saline (14.4%) on tracheal mucus velocity (TMV) in the anaesthetised spontaneously breathing guinea-pig

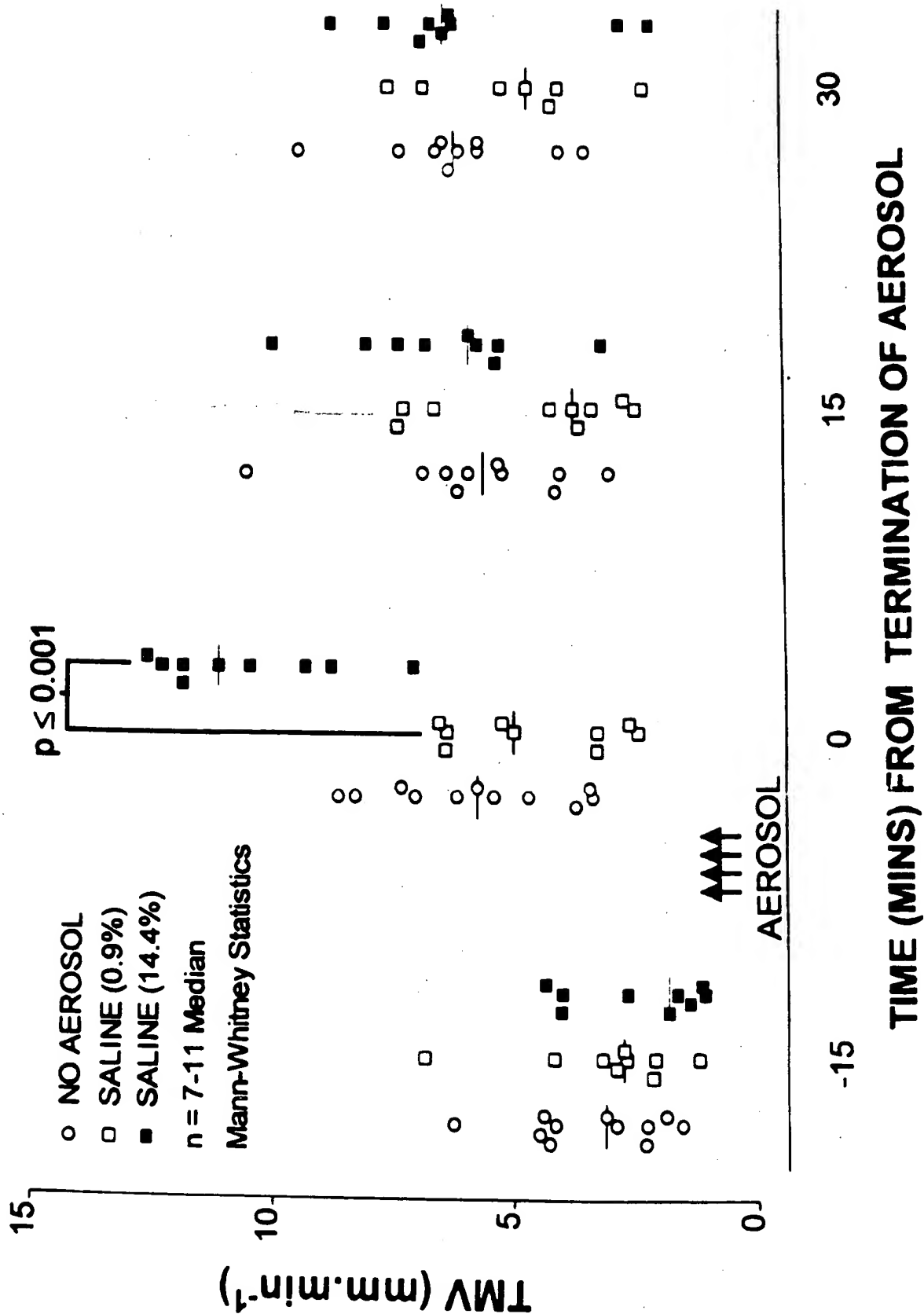
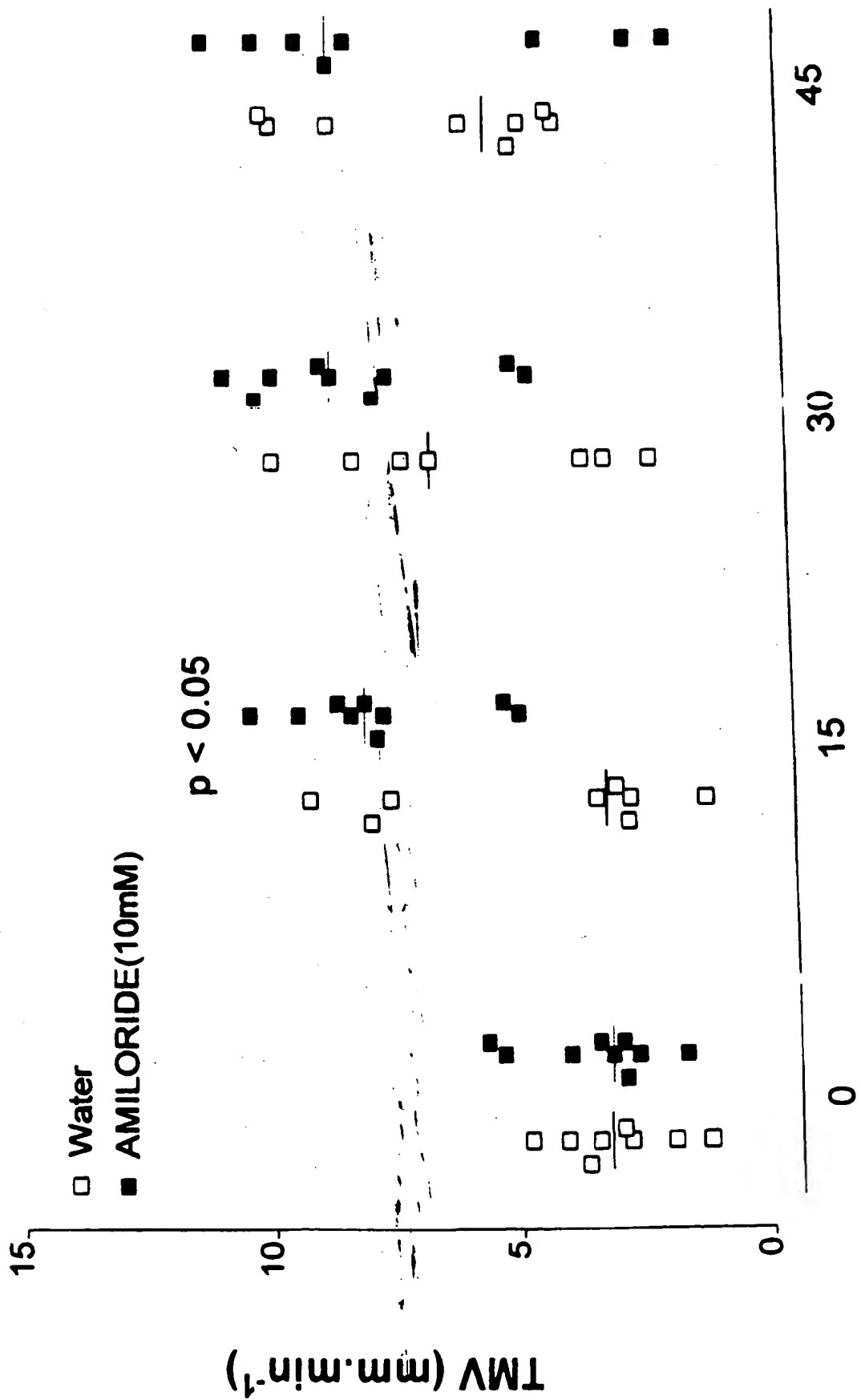


Figure 19 : The effect of a 20 min aerosol of amiloride (10mM) on tracheal mucus velocity (TMV) in the anaesthetised spontaneously breathing guinea-pig



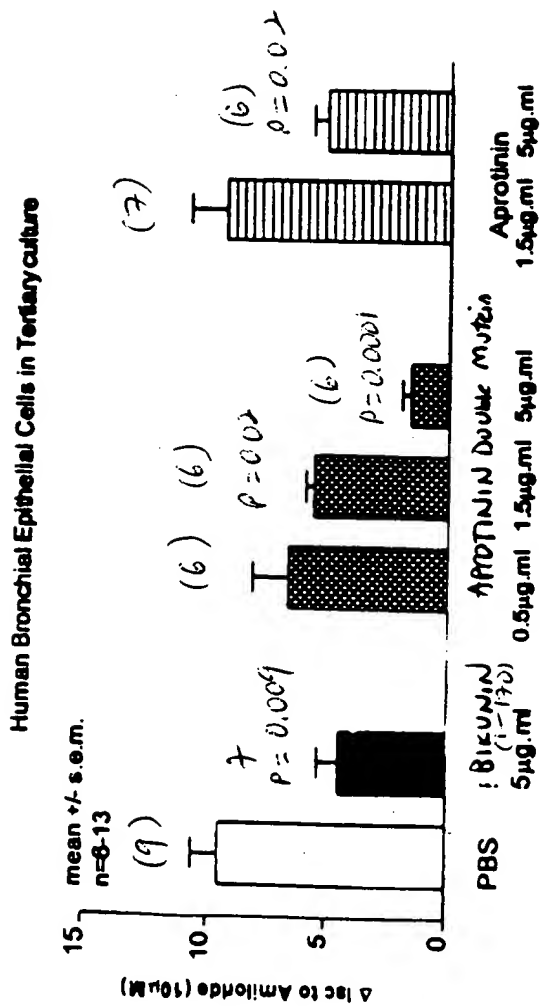


Figure 20 : Aprotinin double mutein (0.5 - 5 ug/mL), Bikunin (1-170) (5ug/mL) and Aprotinin (5 ug/mL) inhibit sodium dependent short circuit current (Isc) in normal human bronchial epithelial cells in vitro at 90 minutes following treatment.

Figure 2) Short circuit current (Isc) trace to show the action of aprotinin (1 mg/mL) on sodium dependent current in cultured cystic fibrosis human bronchial epithelial cells in vitro

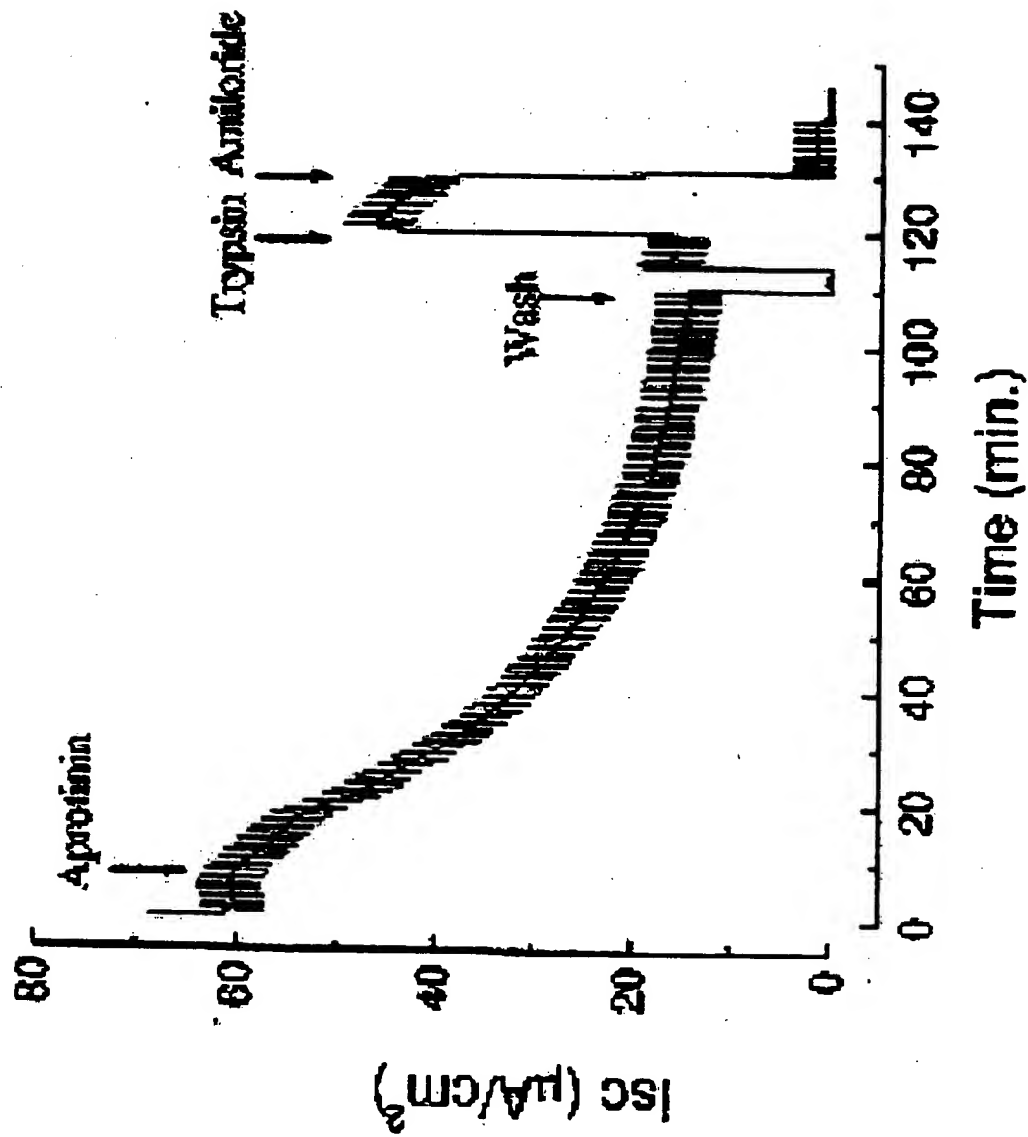


Figure 22 : 9mg CHO rhBikunin (1-170) aerosol (3 mL of 3 mg/mL) increased tracheal mucus velocity in sheep (n=6) at 0, 0.5, 3, 4, 5, 6, 7 & 8 hour time points compared to animals (n=6) receiving PBS vehicle aerosol

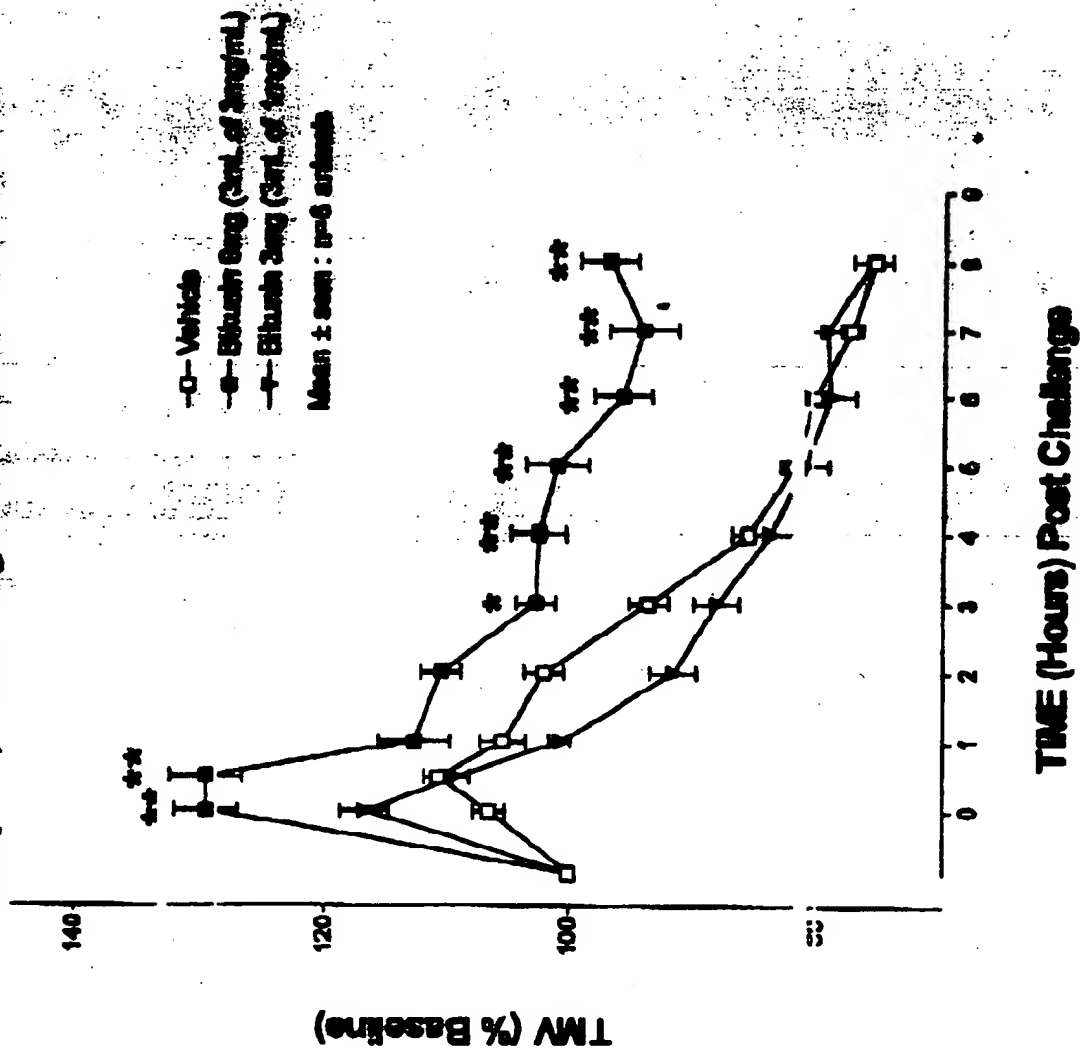


Figure 23 : The effect of a 30 minute pre-treatment of Bikunin (50 and 10 ug/mL) on the short circuit current (Δ Isc) response to amiloride (30uM) in cultured guinea-pig tracheal epithelial cells

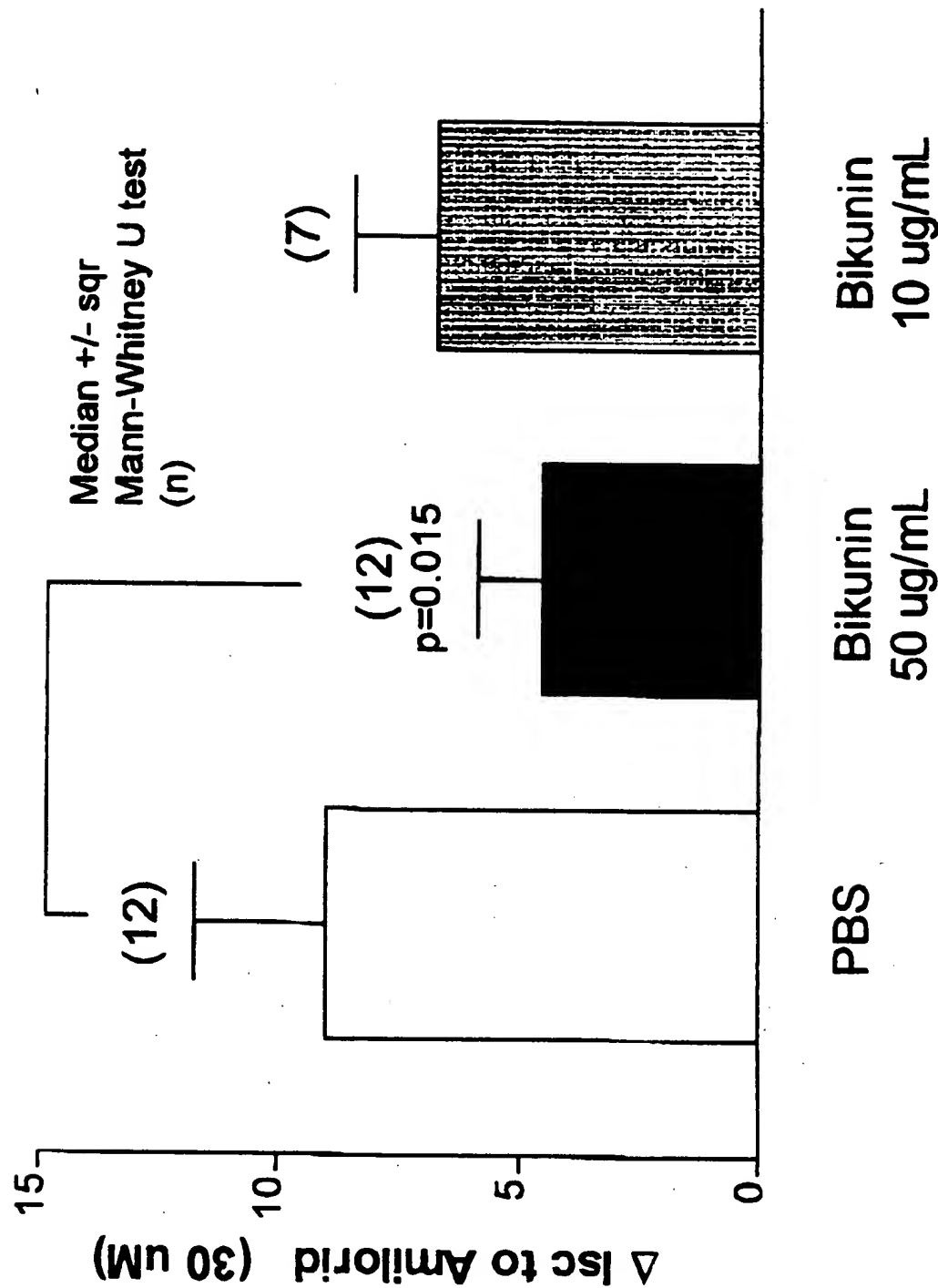


Figure 24 : The effect of a 90 minute pre-treatment of Bikunin (100 and 50 ug/mL) on the short circuit current (Δ Isc) response to amiloride (10 uM) in cultured Ovine tracheal epithelial cells

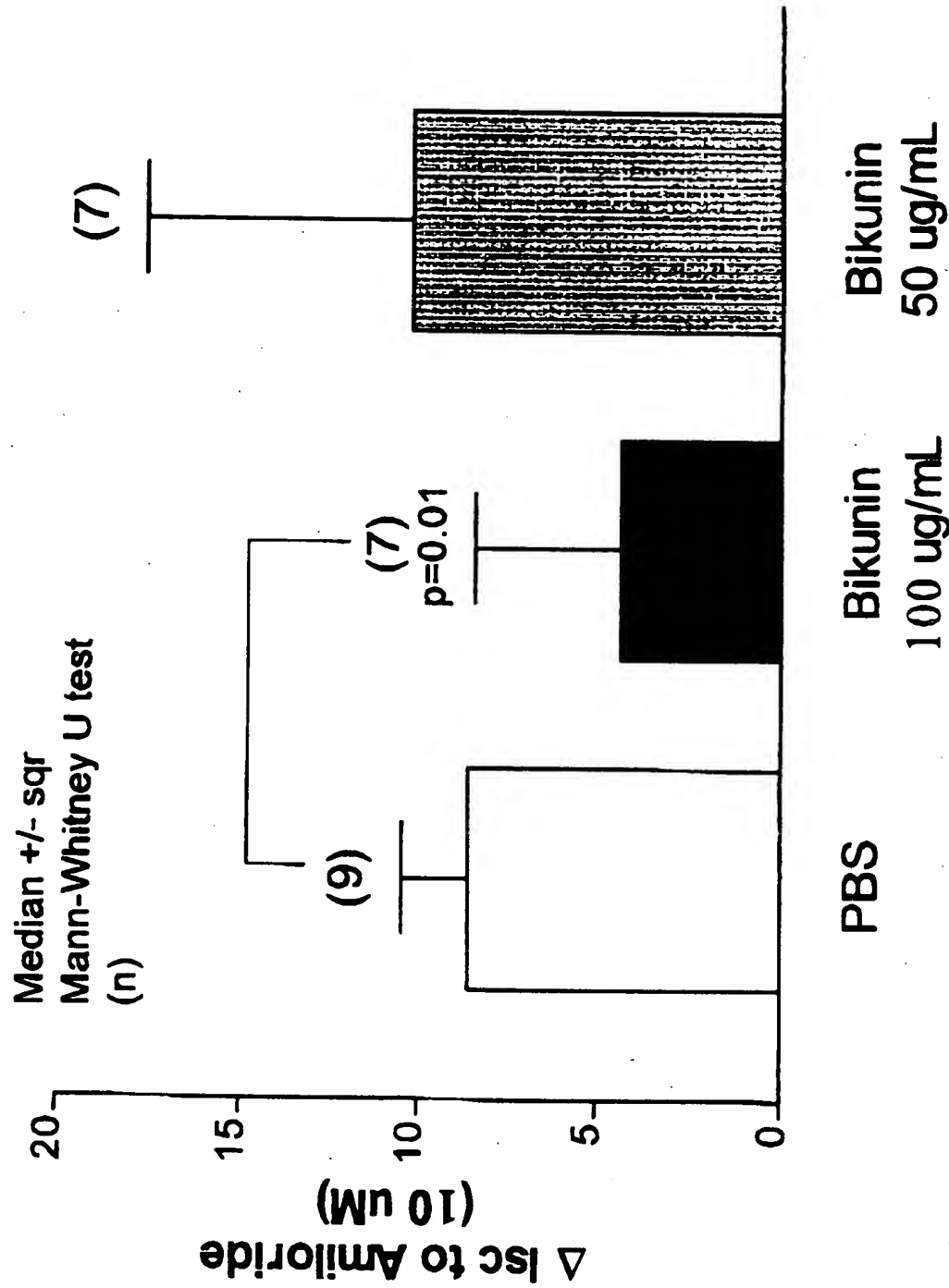


Figure 2(4): The Effect of LPS (0.03 mg/mL x 10 min) on neutrophil numbers in bronchoalveolar lavage fluid (BALF) of the guinea-pig 24 hours post challenge

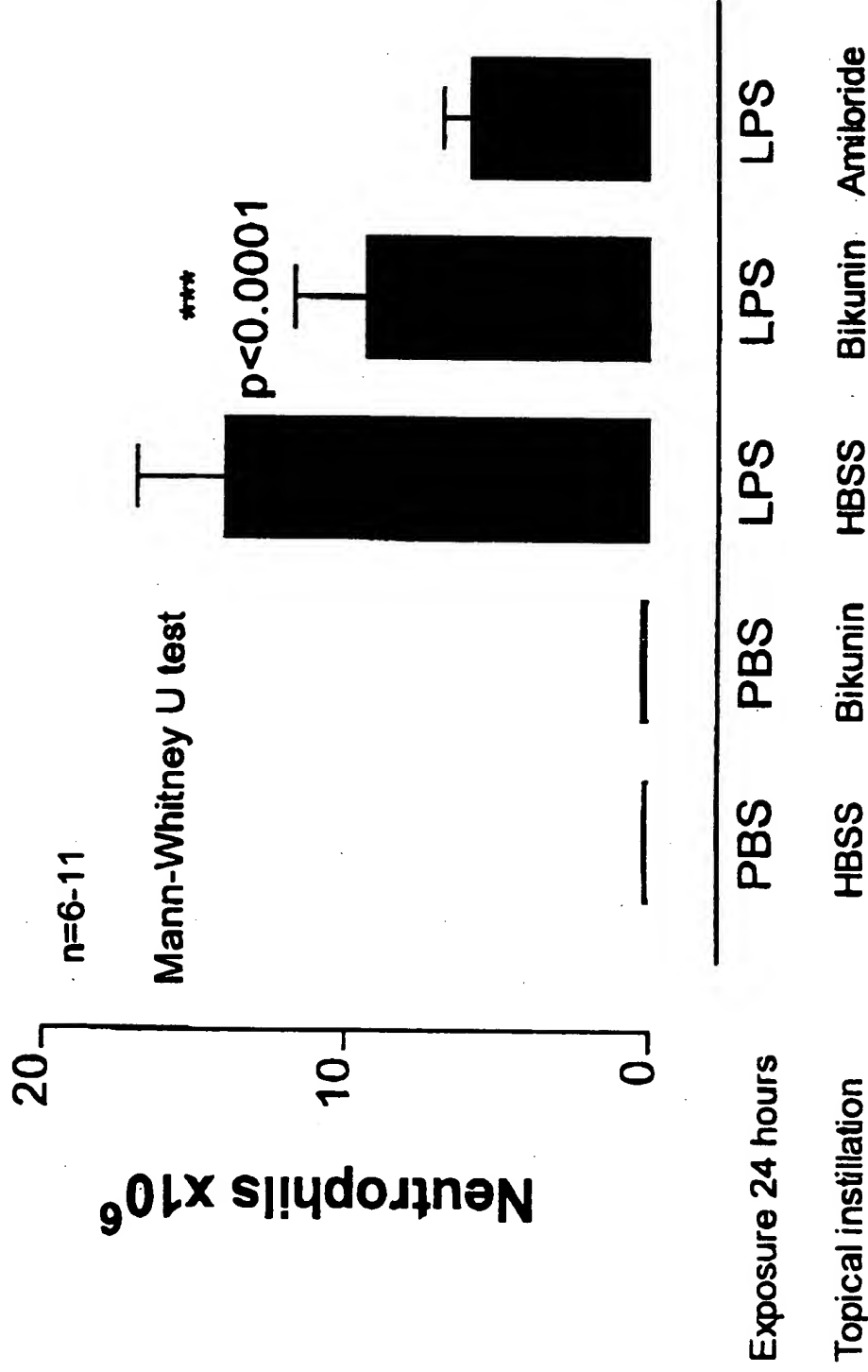
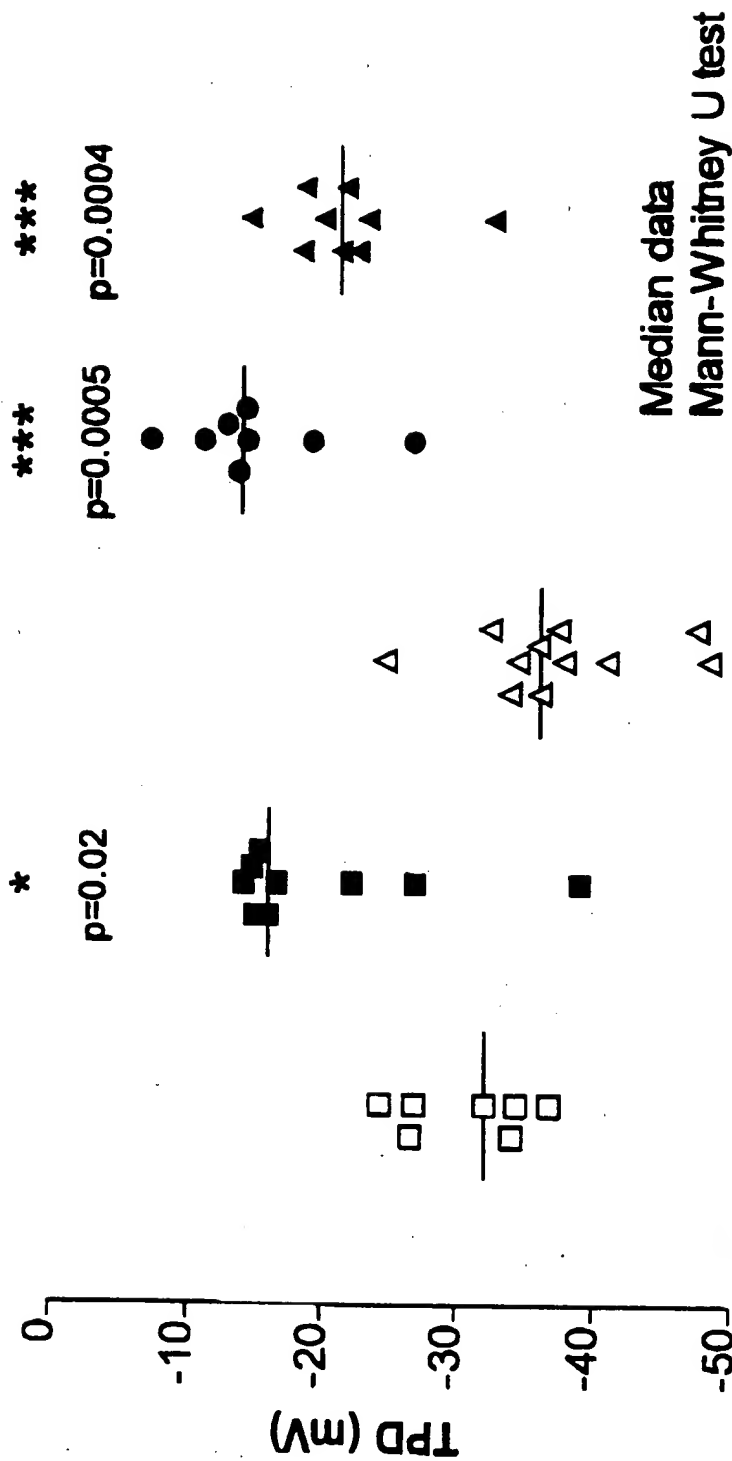
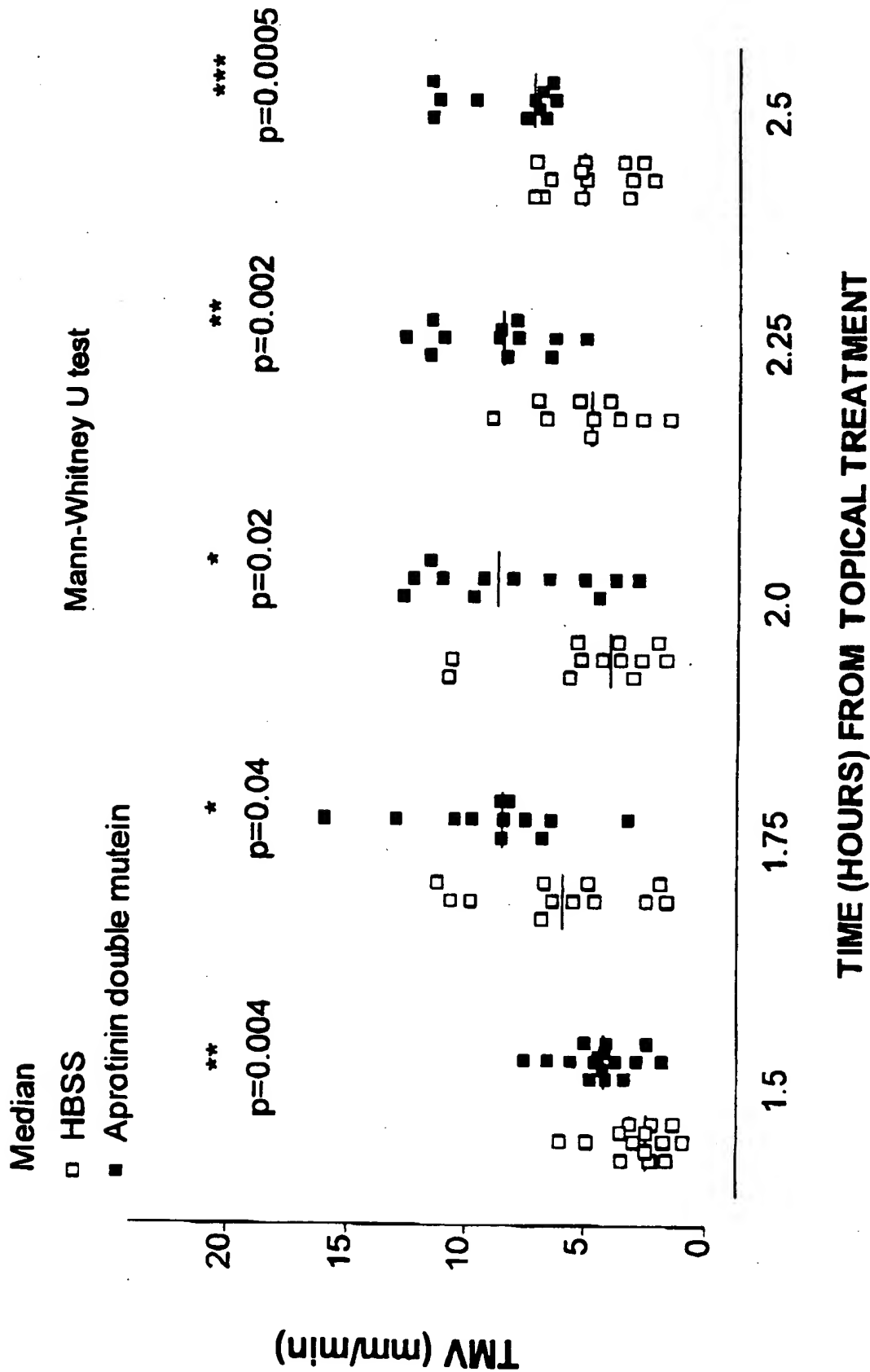


Figure 25(4) : The Effect of Bikunin (50 ug/mL) on Tracheal Potential Difference (TPD) in Guinea-Pigs pre-exposed to LPS (0.03 mg/mL x 10 min)



Exposure - 24 hours	PBS	HBSS	LPS	LPS + Bikunin
Topical instillation	HBSS	Bikunin	HBSS	Amitoride (100 uM)

Figure 26: The effect of Aprotinin double mutein (10 ug) on tracheal mucus velocity (TMV) in the anaesthetised spontaneously breathing guinea-pig



57

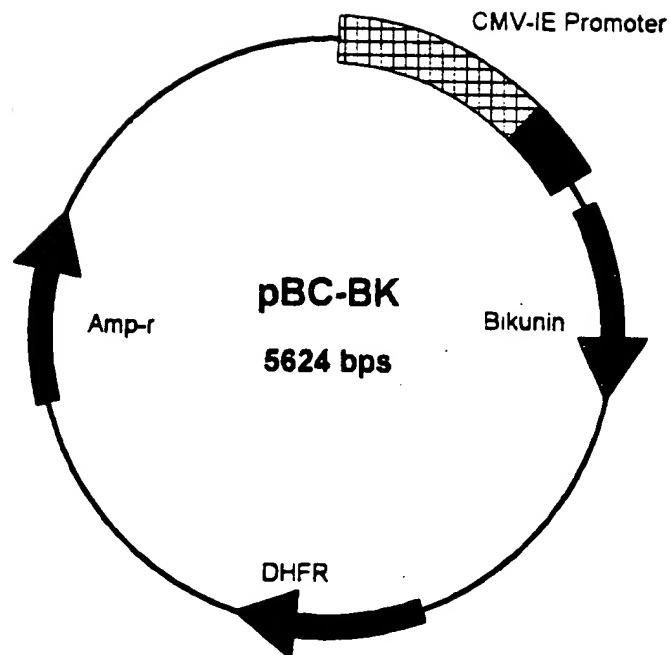
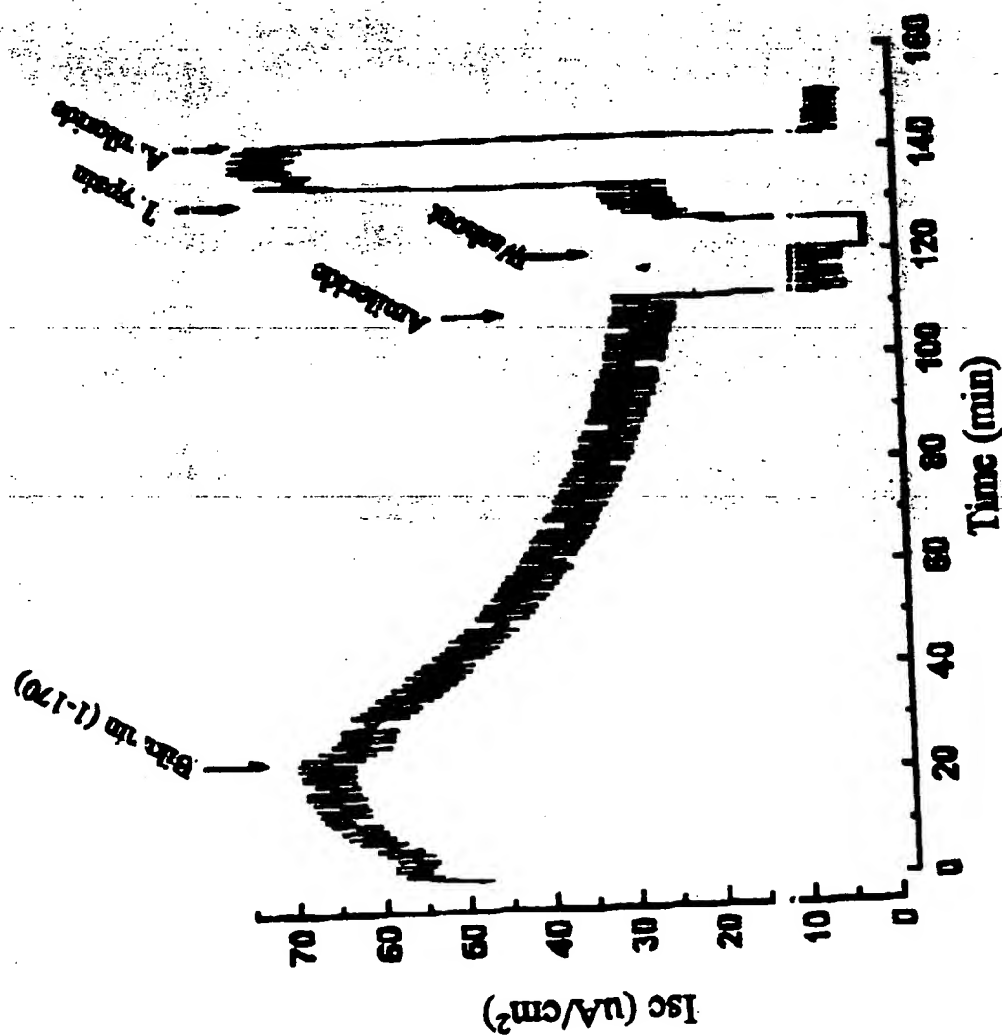


Figure 27

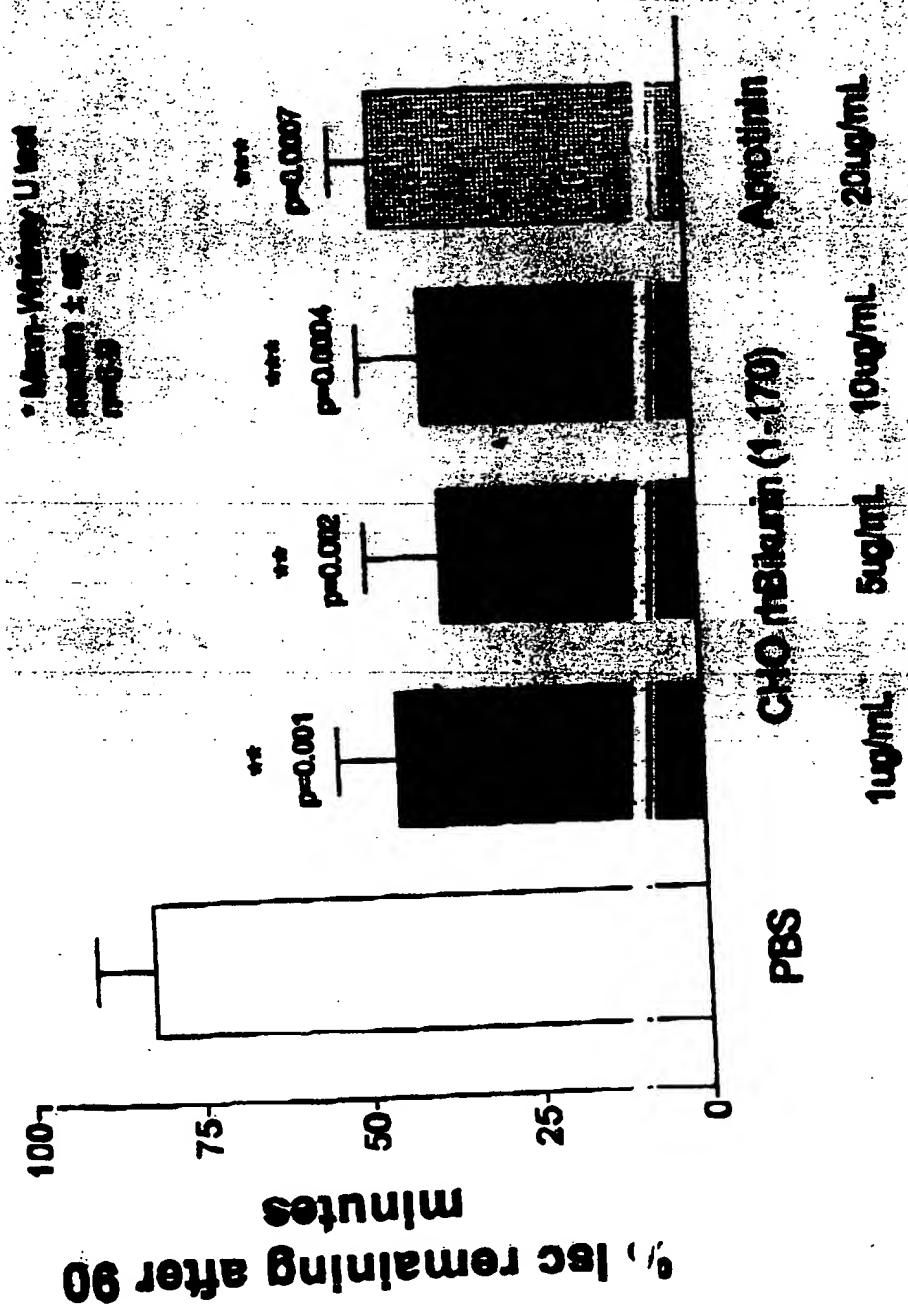
58

Figure 28(a): Short circuit current (Isc) trace to show the action of CHO rhBikunin (1-170) (10 ug/mL) on sodium dependent current in cultured cystic fibrosis human bronchial epithelial cells in vitro.



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Figure 28(b) : Percentage baseline short circuit current (I_{sc}) remaining at 90 minutes after pretreatment with PBS, CHO rhBikunin (1-170) (1.0 ug/mL - 10 ug/mL) or Aprotinin (20 ug/mL) in cystic fibrosis bronchial epithelial cells in vitro.



60

Flow Chart of CHO rhBikunin Purification Process Train

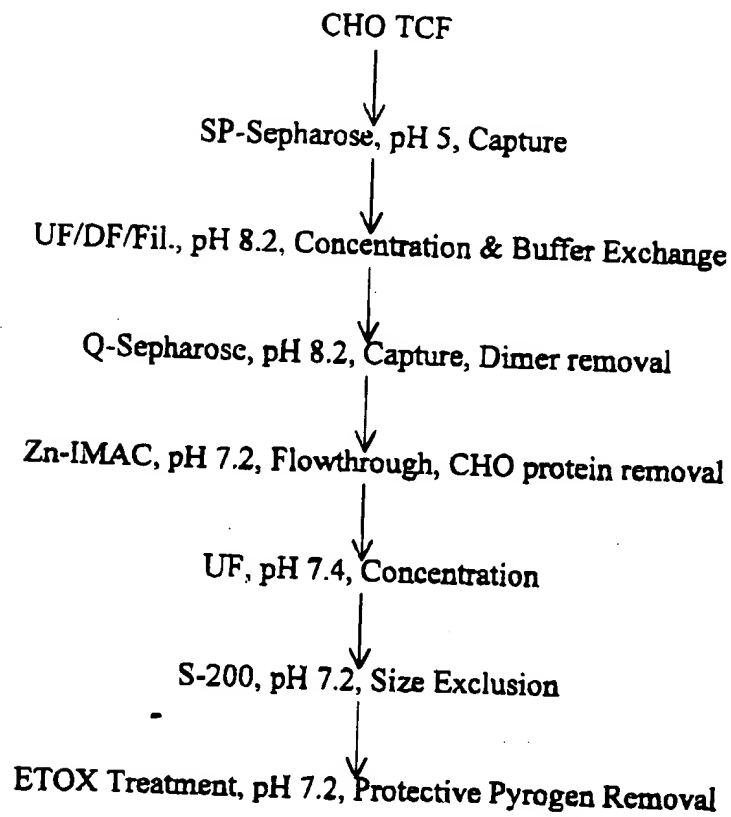
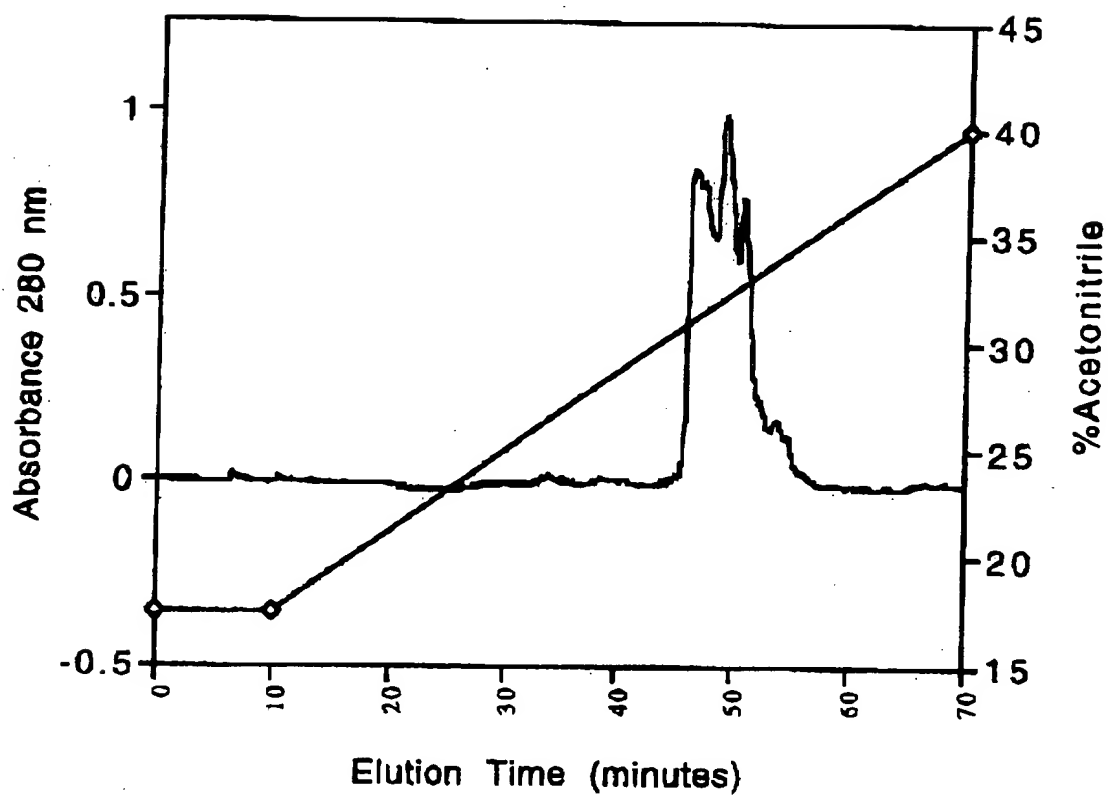


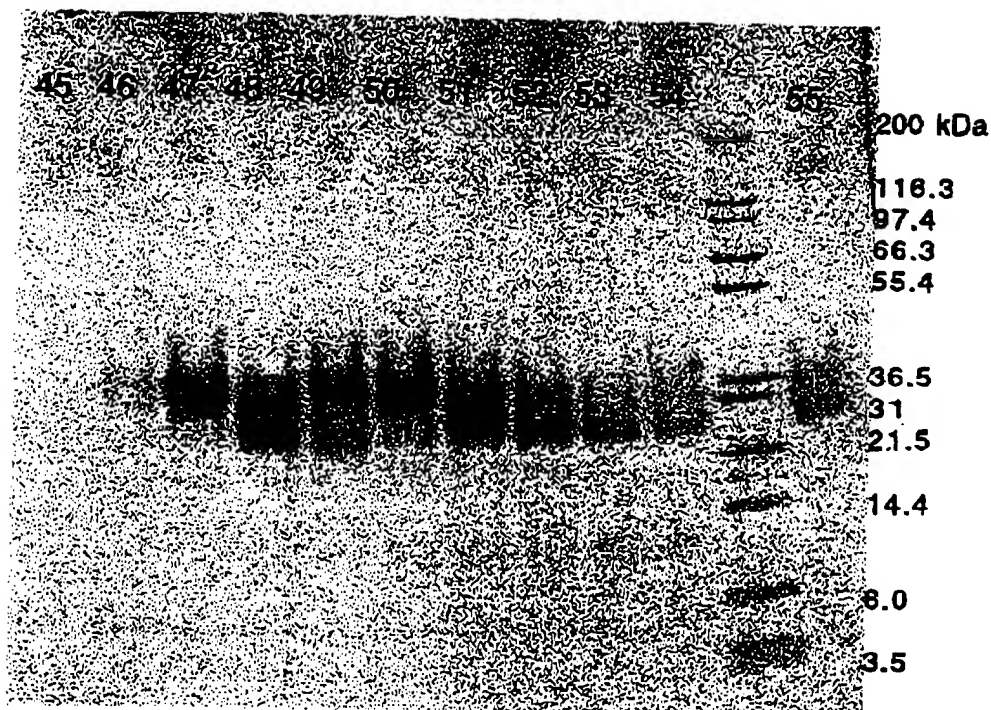
Figure 29

Figure 30(a)



62

Figure B 30(b)

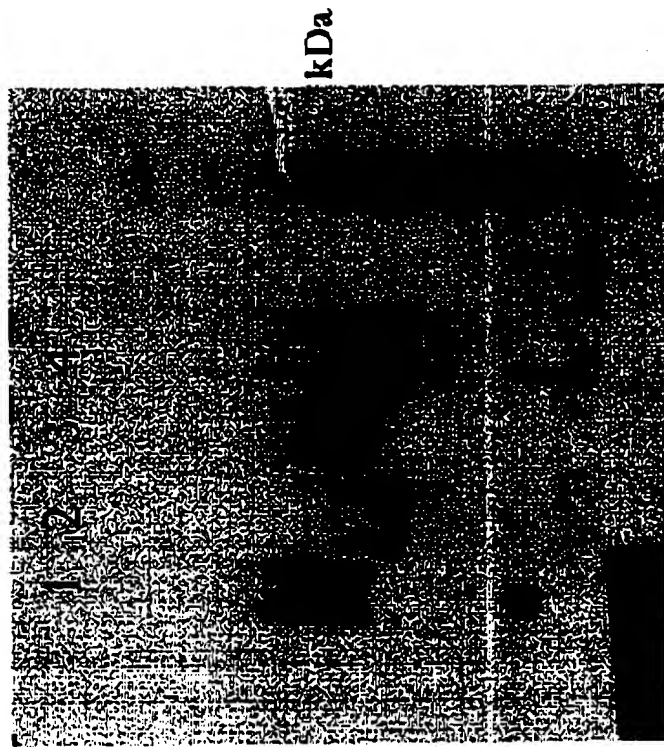


001106-1199

66711-9911150

Figure 31

Deglycosylation of CHO-derived Bikunin



- Lane 1: "High" MW bikunin prior to treatment
2: "High" MW bikunin post N-Glycosidase F
3: "Low" MW bikunin prior to treatment
4: "Low" MW bikunin post N-Glycosidase F